

GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: August 4, 2004, 02:35:09 ; Search time 19705 Seconds  
(without alignments)  
11620.464 Million cell updates/sec

Title: US-09-921-143-36

Perfect score: 5283

Sequence: 1 aagctgacattatgcgact.....tgagtgttcggcagcggtg 5283

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 3470272 seqs, 21671516995 residues

Total number of hits satisfying chosen parameters: 6940544

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

GenEmbl.\*

1: gb.ba.\*

2: gb.htg.\*

3: gb.in.\*

4: gb.om.\*

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35: em.htg.rod.\*

36: em.htg.man.\*

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40: em.htgo.mus.\*

41: em.htgo.other.\*

score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	2410	45.6	6074	12	CVE18316
2	2240	42.4	8349	6	AR260588
3	2233.4	42.3	2661	12	SYN8KMRG
4	2218.4	42.0	2999	12	SYNCCDBA
5	2218.4	42.0	2999	12	SYNCCDBB
6	2177.4	41.2	2604	12	AY189826
7	2177.4	41.2	11373	12	AY189827
8	2177.4	41.2	11403	12	AY189829
9	2088.4	39.5	3036	12	AY222815
10	2088.4	39.5	3210	12	AY219859
11	2088.4	39.5	5695	12	AY222822
12	2088.4	39.5	5869	12	AY219861
13	2088	39.5	5695	12	AF445080
14	2078	39.3	3035	12	AY222814
15	2078	39.3	3053	12	AY222811
16	1892	35.8	7020	12	AS293724
17	1793.4	33.9	4800	6	AR282049
18	1730.2	32.8	7414	12	AF402295
19	1692.4	32.0	5225	6	AX226280
20	1671.2	31.6	5041	12	PKSM713
21	1671.2	31.6	5041	12	PKSM715
22	1671	31.6	4359	12	AY219686
23	1671	31.6	4968	12	AY219687
24	1671	31.6	7018	12	AY219683
25	1669.6	31.6	5025	12	EC07659
26	1652.4	31.3	5594	6	AR214682
27	1644.6	31.1	2959	12	AF402779
28	1625.6	30.8	3741	12	PKSM711
29	1618.2	30.6	6561	6	AR214683
30	1603.8	30.4	3599	6	BD063790
31	1603.8	30.4	3599	6	BD069041
32	1602.2	30.3	3600	6	BD063789
33	1602.2	30.3	3600	6	BD069040
34	1600	30.3	5966	6	BD136050
35	1572.6	29.8	8363	12	AF098284
36	1571.6	29.7	4665	6	AR127825
37	1571.6	29.7	4665	6	AR344433
38	1571.6	29.7	4665	6	BD082038
39	1570.8	29.7	5063	6	BD139247
40	1570	29.7	4517	6	E59418
41	1570	29.7	4518	6	AR214679
42	1570	29.7	4518	12	XXU37573
43	1570	29.7	4775	6	AX798196
44	1570	29.7	4886	6	AX214349
45	1570	29.7	5619	6	AX008865

# ALIGNMENTS

RESULT 1	CVE18316	Cloning vector pKGM1.	6074 bp	DNA	linear	SYN 02-SEP-1999
LOCUS	CVE18316	Cloning vector pKGM1.	6074 bp	DNA	linear	SYN 02-SEP-1999
DEFINITION	Y18316					
ACCESSION	Y18316.1	GI:5830187				
VERSION	Y18316.1	GI:5830187				
KEYWORDS	bleomycin resistance; cloning vector; kanamycin resistance; multiple cloning site; neomycin resistance.					
SOURCE	Cloning vector pKGM1					
ORGANISM	Cloning vector pKGM1					
REFERENCE	artificial sequences; vectors.					
AUTHORS	1					
TITLE	Bannasch,D. and Schwab,M.					
JOURNAL	A versatile bait vector for rapid Gal4 dependent two-hybrid screens					
	Unpublished					

Pred. No. is the number of results predicted by chance to have a

REFERENCE	2	(bases 1 to 6074)
AUTHORS	Bannasch, D.	
TITLE	Direct Submission	
JOURNAL	Submitted (30-OCT-1998) D. Bannasch, Institutium Division of, Cyto genetics/H0400 Deutsches, Krebsforschungszentrum (DKFZ), Im Neuenheimer Feld 280, D-69120 Heidelberg, FRG	
REMARK	Revised by author 10-JUN-1999	
COMMENT	Related sequences U07646, U00004, L19385.	
FEATURES	Location/Qualifiers	
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	/mol_type="other DNA"	
	/db_xref="taxon:91498"	
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	/protein_id="CAB54527.1"	
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	/translation="MKLISIEQACDICRLKLLKCSKEPKCAKCLKNWCEKRSYPT KRSPLRAHTEFVESRLERLEQFLIFREDLDMLKMSLDQIKALLTGLFVQDNV NKAQVDRLASVETDMLTQRHRSATSSSESSNKQRLTVSPFQFVRIIRRP AAKLIQGEFLMIYDFYY"	
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misc_feature	877..905	
	/note="multiple cloning site"	
CDS	complement(3126..3506)	
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	/product="bleomycin resistance protein"	
	/protein_id="CAB54529.1"	
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gene	complement(4410..4459)	
	/gene="aminoglycoside phosphotransferase"	
promoter	complement(4410..4459)	
	/gene="aminoglycoside phosphotransferase"	
ORIGIN		
Query Match	45.6%;	Score 2410; DB 12; Length 6074;
Best Local Similarity	94.5%;	Prod. No. 0;
Matches 2568; Conservative	5;	Mismatches 145; Gaps 1;
QY	2711	CGTAATCATGGTCATAGCTGTTTCTGTGTGAAATTGTTATCCGCTCACAAATCCACACA 2770
Db	1954	CGTAATCATGGTCATAGCTGTTTCTGTGTGAAATTGTTATCCGCTCACAAATCCACACA 2013
QY	2771	ACATACGACCGGAAGCATAAAGTCTTAAGCCTGGGTGCGCTAATGAGTGAGCTAACTCA 2830
Db	2014	ACATACGACCGGAAGCATAAAGTCTTAAGCCTGGGTGCGCTAATGAGTGAGTGAGCTCA 2073
QY	2831	CATTAAATTCGGTTGGCTCACTGCCCGCTTTCAGTCGGGAAACCTGTCGTCGACGCTGC 2890
Db	2074	CATTAAATTCGGTTGGCTCACTGCCCGCTTTCAGTCGGGAAACCTGTCGTCGTCGACGCTGC 2133
QY	2891	ATTAAATGAATCGGCAACCGCGGGGAGGAGCGGTTTCGTTATTGGGCGCTCTTCGCGTT 2950
Db	2134	ATTAAATGAATCGGCAACCGCGGGGAGGAGCGGTTTCGTTATTGGGCGCTCTTCGCGTT 2139

QY	3886	GATTTGCACTGCGGTAGAACTCCGCGAGGTGCTCCAGCCTCAGCGACGAGCTGAACAA	3945	Db	4354	ATCTTGATCCCTGCGCATCAGATCCTTGGGGCAAGAAAGCATTCAGTTTACTTTGC	4413
Db	3274	GATTTGCACTGCGGTAGAACTCCGCGAGGTGCTCCAGCCTCAGCGACGAGCTGAACAA	3333	QY	5026	AGGCTTCCCAACCTTACAGAGGCGCCCGAGTGGCAATTCGGTTTCGCTTGTGTCC	5085
QY	3946	CTCGAGGGGATCAGAGCCCGGGTGGCGAAGAACTCCAGCATGAGATCCCGCGCTGG	4005	Db	4414	AGGCTTCCCAACCTTACAGAGGCGCCCGAGTGGCAATTCGGTTTCGCTTGTGTCC	4473
Db	3334	CTCGAGGGGATCAGAGCCCGGGTGGCGAAGAACTCCAGCATGAGATCCCGCGCTGG	3393	QY	5086	ATAAAACCGCCAGTCTAGCTATCGCCATGTAAGCCCACTGAAGCTACCTTCTCT	5145
QY	4006	AGGATCATCCAGCGCGCTCCCGGAAACGATTCGGAAGCCCACTTTCATAGAAGCG	4065	Db	4474	ATAAAACCGCCAGTCTAGCTATCGCCATGTAAGCCCACTGAAGCTACCTTCTCT	4533
Db	3394	AGGATCATCCAGCGCGCTCCCGGAAACGATTCGGAAGCCCACTTTCATAGAAGCG	3453	QY	5146	TTGCGCTTGCCTTTCCCTTGTCCAGATAGCCAGTAGCTGACATTCATCCGGGTGAG	5205
QY	4066	GCGTGGAAATCGAATCTCGTATGAGCGAGTTGGCGTTCGCTTGGTTCGATTCGAAC	4125	Db	4534	TTGCGCTTGCCTTTCCCTTGTCCAGATAGCCAGTAGCTGACATTCATCCGGGTGAG	4593
Db	3454	GCGTGGAAATCGAATCTCGTATGAGCGAGTTGGCGTTCGCTTGGTTCGATTCGAAC	3513	QY	5206	ACCGTTTCTGCGGACTGGCTTTCAGGTTCGCTTCCCTTTAGCAGCCCTTGGCCCTG	5265
QY	4126	CCCAGAGTCCCGCTCAGAAAGAACTCGTCAAGAGCGGATAGAGCGGATGCGTCCGAT	4185	Db	4594	ACCGTTTCTGCGGACTGGCTTTCAGGTTCGCTTCCCTTTAGCAGCCCTTGGCCCTG	5265
Db	3514	CCCAGAGTCCCGCTCAGAAAGAACTCGTCAAGAGCGGATAGAGCGGATGCGTCCGAT	3573	QY	5266	AGTCTTTCGCGCAGCGTG	5283
QY	4186	CGGAGCGGCGATACCGTAAAGCAAGAGAGCGGTGAGCCATTCGCGCCAAAGCTCTT	4245	Db	4654	AGTCTTTCGCGCAGCGTG	4671
Db	3574	CGGAGCGGCGATACCGTAAAGCAAGAGAGCGGTGAGCCATTCGCGCCAAAGCTCTT	3633	RESULT 2			
QY	4246	CAGCAATATCAGCGGTAGCCAAAGCTATGCTGATAGCGTCCGCAACCCAGCGCG	4305	AR260588	8349 bp	DNA	linear
Db	3634	CAGCAATATCAGCGGTAGCCAAAGCTATGCTGATAGCGTCCGCAACCCAGCGCG	3693	LOCUS	Sequence 16 from patent US 6489542.		PAT 20-DEC-2002
QY	4306	CACAGTCCGATGAATCCAGAAAGCGGCAATTTCCACCATGATATTCGGCAAGCAGCAT	4365	DEFINITION	AR260588		
Db	3694	CACAGTCCGATGAATCCAGAAAGCGGCAATTTCCACCATGATATTCGGCAAGCAGCAT	3753	ACCESSION	AR260588.1	GI:27311143	
QY	4366	CGCATCGGTACGACGAGATCTTCGCGTGGCGATGCGCGCTTGAGCTGCGGAACA	4425	VERSION	AR260588.1	GI:27311143	
Db	3754	CGCATCGGTACGACGAGATCTTCGCGTGGCGATGCGCGCTTGAGCTGCGGAACA	3813	KEYWORDS			
QY	4426	GTTCGGTGGCGGAGCCCTGATGCTCTTCGTCAGATATCTGATGACAAAGACCGG	4485	SOURCE	Unknown.		
Db	3814	GTTCGGTGGCGGAGCCCTGATGCTCTTCGTCAGATATCTGATGACAAAGACCGG	3873	ORGANISM	Unclassified.		
QY	4486	CTTCCATCCGAGTACGTGCTCGCTCGATGCGATGTTTCGCTGCTGCTGCTGCTGCTG	4545	REFERENCE	1. (bases 1 to 8349)		
Db	3874	CTTCCATCCGAGTACGTGCTCGCTCGATGCGATGTTTCGCTGCTGCTGCTGCTGCTG	3933	AUTHORS	Corbin,D.R. and Romano,C.P.		
QY	4546	TAGCGGATCAAGGTATGACGCGCGCGATTCGATCAGCCATGATGATATCTTCGCG	4605	TITLE	Methods for transforming plants to express Cry2Ab		
Db	3934	TAGCGGATCAAGGTATGACGCGCGCGATTCGATCAGCCATGATGATATCTTCGCG	3993	JOURNAL	delta.-endotoxins targeted to the plastids		
QY	4606	CAGGACAGGTGAGATGACAGGAGATCTTCGCGCGCGCACTTCGCCCAATAGCAGCAGT	4665	FEATURES	Patent: US 6489542-A 16 03-DEC-2002;		
Db	3994	CAGGACAGGTGAGATGACAGGAGATCTTCGCGCGCGCACTTCGCCCAATAGCAGCAGT	4053	source	Location/Qualifiers		
QY	4666	CCCTTCCCGCTTCAGTGACAAAGCTCGAGCAAGTGGCGATGCGCGCTTGAGCTGCGGAACA	4725	mol_type="genomic DNA"			
Db	4054	CCCTTCCCGCTTCAGTGACAAAGCTCGAGCAAGTGGCGATGCGCGCTTGAGCTGCGGAACA	4113	Query Match	42.4%; Score 2240; DB 6; Length 8349;		
QY	4726	GCACGATAGCGCGTGCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	4785	Best Local Similarity	93.4%; Pred. No. 0;		
Db	4114	GCACGATAGCGCGTGCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	4173	Matches	2409; Conservative 0; Mismatches 25; Indels 144; Gaps 1;		
QY	4786	TGACAAAAGAACCGGGCGCCCTTCGCTGACAGCGGAAACCGCGGCGATCAGAGCAGC	4845	QY	2706	CTAGAGCTAATCATGTTCATAGCTGTTTCTGCTGTGAATTTGTTATCCGCTCAATTC	2765
Db	4174	TGACAAAAGAACCGGGCGCCCTTCGCTGACAGCGGAAACCGCGGCGATCAGAGCAGC	4233	Db	5911	CTTGGCGTAAATCATGTTCATAGCTGTTTCTGCTGTGAATTTGTTATCCGCTCAATTC	5970
QY	4846	CGATTGCTGTTGTGCCAGTATAGCGAATAGCTCTTCCACCCAAAGCGCGCGAGAAC	4905	QY	2766	ACACACATACGAGCGGAGCATTAAGTGAAGCTGGGGTGCCTTAATGAGTACGCTA	2825
Db	4234	CGATTGCTGTTGTGCCAGTATAGCGAATAGCTCTTCCACCCAAAGCGCGCGAGAAC	4293	Db	5971	ACACACATACGAGCGGAGCATTAAGTGAAGCTGGGGTGCCTTAATGAGTACGCTA	6030
QY	4906	CTGCGTGCAATCATCTTGTTCATCATCGAAACGATCCTCATCTCTCTTGTATCAG	4965	QY	2826	ACTCACATTAATTCGCTTGGCTCACTGCCCGCTTCCAGTCGGGAAACCTGCTGCCA	2885
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QY	4966	ATCTTGATCCCTTGCCCATCAGATCTTGGCGGCAAGAAAGCCATCCAGTTTACTTTGC	5025	QY	2886	GTTGCAATTAATTCGCTTGGCTCACTGCCCGCTTCCAGTCGGGAAACCTGCTGCCA	2945
				Db	6091	GTTGCAATTAATTCGCTTGGCTCACTGCCCGCTTCCAGTCGGGAAACCTGCTGCCA	6150
				QY	2946	CGCTTCTCGCTCACTGACTCGCTGCGCTCGGTTCGCTTCCGCTGCGGCGAGCGGTATCAG	3005
				Db	6151	CGCTTCTCGCTCACTGACTCGCTGCGCTCGGTTCGCTTCCGCTGCGGCGAGCGGTATCAG	6210
				QY	3006	TCACTCAAGGCGGTAAATGAGGTTATCAGAGTACAGGAGTAAACGAGGAAAGAAAT	3065
				Db	6211	TCACTCAAGGCGGTAAATGAGGTTATCAGAGTACAGGAGTAAACGAGGAAAGAAAT	6270

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Db	6271	GTAGCAAAAAGCCAGCAAAAAGCCAGGAAACCGTAAAAAGCCCGCTTGTCTGGCGTTTTT	6330	QY	4206	AGCAGAGGAGCGGTAGCCCATTCGCGCCCAAGCTCTTCAGCAATATCAGCGGTAGCC	4265
QY	3126	CCATAGGCTCCGCCCTCGAGAGCATCACAAAATCGAGCTCAAGTCAGAGGTGGCG	3185	Db	7267	AGCAGAGGAGCGGTAGCCCATTCGCGCCCAAGCTCTTCAGCAATATCAGCGGTAGCC	7326
Db	6331	CCATAGGCTCCGCCCTCGAGAGCATCACAAAATCGAGCTCAAGTCAGAGGTGGCG	6390	QY	4266	AACGCTATGCTCTGATAGCGGTCCGCCACACCCAGCCGCCACACGTCGATGAATCCAGAA	4325
QY	3186	AAACCCGACAGGACTATAAGATACAGCGGTTTTCCCCCTGGAAGCTCCCTCGTGGCTC	3245	Db	7327	AACGCTATGCTCTGATAGCGGTCCGCCACACCCAGCCGCCACACGTCGATGAATCCAGAA	7386
Db	6391	AAACCCGACAGGACTATAAGATACAGCGGTTTTCCCCCTGGAAGCTCCCTCGTGGCTC	6450	QY	4326	AAGCGCGCATTTTCCACCATGATATTCCGCAAGAGGCAATCCCATGGGTACAGAGAGA	4385
QY	3246	TCCTGTTCCGACCTCGCGCTTACCGGATACCTGTCCGCTTTCTCCCTTCGGGAAGGT	3305	Db	7387	AAGCGCGCATTTTCCACCATGATATTCCGCAAGAGGCAATCCCATGGGTACAGAGAGA	7446
Db	6451	TCCTGTTCCGACCTCGCGCTTACCGGATACCTGTCCGCTTTCTCCCTTCGGGAAGGT	6510	QY	4386	TCCTCGCGTCCGGGATCGCGGCTTGGCTGGCGAAGTTCGGCTGGCGCGAGCCCC	4445
QY	3306	GGCGCTTCTCATAGCTACGCTGAGGTATCTCAGTTCCGTTGAGTGTGGTTCGGTCCAA	3365	Db	7447	TCCTCGCGTCCGGGATCGCGGCTTGGCTGGCGAAGTTCGGCTGGCGCGAGCCCC	7506
Db	6511	GGCGCTTCTCATAGCTACGCTGAGGTATCTCAGTTCCGTTGAGTGTGGTTCGGTCCAA	6570	QY	4446	TCGATCTCTTCGTTCCAGATCATCTCTGATCGAACAAGACCGGCTTCCATCCGAGTACGTGT	4505
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Db	6571	GCTGGGCTGTGTGCACGAACCCCGCTTCAGCCCGACCGCTGCGCTTATCCGGTAACTA	6630	QY	4506	CGCTCGATCGATGTTTTCGTTGGTGGTTCGAATGGGCAAGGTAGCGAGTACCGGATGATGC	4565
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Db	6631	TCGCTTTGAGTCCAAACCCCGTAAAGACAGCACTTATCGCACTGGCAGAGCCACTGGTAA	6690	QY	4566	AGCGCGCATTTGCATCAGCCATGATGATCTTCTCGGAGGAGCAAGGTAGATGAC	4625
QY	3486	CAGGATTACAGAGCAGGTATGTAGCGGTGCTACAGAGTTCTTCAAGTGGTGGCTTAA	3545	Db	7627	AGCGCGCATTTGCATCAGCCATGATGATCTTCTCGGAGGAGCAAGGTAGATGAC	7686
Db	6691	CAGGATTACAGAGCAGGTATGTAGCGGTGCTACAGAGTTCTTCAAGTGGTGGCTTAA	6750	QY	4626	AGGAGATCTTCCCGCGCACTTCGCCAATAGCAGCCAGTCCCTTCCCGCTTCAGTGA	4685
QY	3546	CTACGGCTACCTAGAGAAACAGTATTGATATCTCGCTCTGCTCAAGCCAGTTACCTT	3605	Db	7687	AGGAGATCTTCCCGCGCACTTCGCCAATAGCAGCCAGTCCCTTCCCGCTTCAGTGA	7746
Db	6751	CTACGGCTACCTAGAGAAACAGTATTGATATCTCGCTCTGCTCAAGCCAGTTACCTT	6810	QY	4686	AGCTCGAGCACAGCTCGCAAGGAAACGCCGCTGCTGGCCAGCAGATAGCCGCGTGCC	4745
QY	3606	CGGAAAAGAGTTGTTAGTCTTGTATCGGCAAAACACCCGCTGGTGGTGGT	3665	Db	7747	AGCTCGAGCACAGCTCGCAAGGAAACGCCGCTGCTGGCCAGCAGATAGCCGCGTGCC	7806
Db	6811	CGGAAAAGAGTTGTTAGTCTTGTATCGGCAAAACACCCGCTGGTGGTGGT	6870	QY	4746	TGCTCTCGAGTTCATTTCAGGCGACCGGACAGTCTTTCGACAAAAGAACCGGCGC	4805
QY	3666	TTTTGTTTCAAGCAGCAGATTACGGCAGAAAAAAGGATCTCAAGAGATCCTTTGAT	3725	Db	7807	TGCTCTCGAGTTCATTTCAGGCGACCGGACAGTCTTTCGACAAAAGAACCGGCGC	7866
Db	6871	TTTTGTTTCAAGCAGCAGATTACGGCAGAAAAAAGGATCTCAAGAGATCCTTTGAT	6930	QY	4806	CCCTCGGCTGACAGCCGGAACACGGCGGATCAGAGCAGCCGATTCGTTGTCGCGAG	4865
QY	3726	CTTTTCTACGGGTCTGACCTCAGTGGAAACGAAACTCAGTTAAGGATTTTGTGAT	3785	Db	7867	CCCTCGGCTGACAGCCGGAACACGGCGGATCAGAGCAGCCGATTCGTTGTCGCGAG	7926
Db	6931	CTTTTCTACGGGTCTGACCTCAGTGGAAACGAAACTCAGTTAAGGATTTTGTGAT	6990	QY	4866	TCATAGCCGAATAGCTCTCCACCAAGCGCGCGAGAACCTCGTGCAATCCATCTGT	4925
QY	3786	GAGATTATCGTCAACAAAGCGGCCATCGTCCCTCCCACTCCTGCAAGTTCCGGGGCATG	3845	Db	7927	TCATAGCCGAATAGCTCTCCACCAAGCGCGCGAGAACCTCGTGCAATCCATCTGT	7986
Db	6991	GAGATTATCAAAAAGGATCTTCACTAGATCCCTT	7024	QY	4926	TCATATCGGAACGATCCTCATCTCTTCGTTGATCAGATCTTTCATCCCTGCGCAT	4985
QY	3846	GATGCGCGGATAGCCGCTGCTGTTTCTTGGATGCGCAGCGAATTGCACTGCGCGTAGAA	3905	Db	7987	TCATATCGGAACGATCCTCATCTCTTCGTTGATCAGATCTTTCATCCCTGCGCAT	8046
Db	7025	-----	7024	QY	4986	CAGATCCTTGGCGGCAAGAAAGCATCCAGTTTACTTTTCAGGGCTTCCCAACTTACCA	5045
QY	3906	CTCCGCGAGTCTGTCAGCCTCAGGACAGCTGAACCAACTCGGAGGGATCGAGCCC	3965	Db	8047	CAGATCCTTGGCGGCAAGAAAGCATCCAGTTTACTTTTCAGGGCTTCCCAACTTACCA	8106
Db	7025	-----	7026	QY	5046	GAGGGGCCCGGAGTGGCAATTCCGGTTCCGTTGCTGTCTTCCATAAACCGCCAGTCTAGC	5105
QY	3966	GGGGTGGCGAAGAACTCCAGCATGAGATCCCGCTGGAGGATCATCCAGCGCGCTC	4025	Db	8107	GAGGGGCCCGGAGTGGCAATTCCGGTTCCGTTGCTGTCTTCCATAAACCGCCAGTCTAGC	8166
Db	7027	GGGGTGGCGAAGAACTCCAGCATGAGATCCCGCTGGAGGATCATCCAGCGCGCTC	7086	QY	5106	TATCGCCATGTAAGCCACCTGCAAGTACCTGCTTCTCTTTGCGCTTGGGTTTTCCTT	5165
QY	4026	CCGGAACAGATTCCGAAGCCCAACCTTTTATAGAAGCGCGGTGGAATCGAAATCTCG	4085	Db	8167	TATCGCCATGTAAGCCACCTGCAAGTACCTGCTTCTCTTTGCGCTTGGGTTTTCCTT	8226
Db	7087	CCGGAACAGATTCCGAAGCCCAACCTTTTATAGAAGCGCGGTGGAATCGAAATCTCG	7146	QY	5166	GTCCAGATAGCCAGTACCTGACATTCATCCGGGTGAGCAGCGGTTCTCGGAGTGGCT	5225
QY	4086	TGATGGAGGTTGGGCTGCTTGGTGGTCAATTCGAAACCCAGAGTCCGCTCAGAG	4145	Db	8227	GTCCAGATAGCCAGTACCTGACATTCATCCGGGTGAGCAGCGGTTCTCGGAGTGGCT	8286
Db	7147	TGATGGAGGTTGGGCTGCTTGGTGGTCAATTCGAAACCCAGAGTCCGCTCAGAG	7206	QY	5226	TTCTACGTGTTCCGCTTCTTTAGCAGCCCTTGGCCCTGAGTCTGCTTGGCGAGCGTG	5283
QY	4146	AACCTCGTCAAGAGGCGATAGAGGCGATGCGTTCGAAATCGGAGCGCGATACCGTAA	4205				





DEFINITION		Cloning vector pKIL18 ccdB gene, complete cds and kanamycin-resistance (KmR) gene fragment.	
ACCESSION	L38498	L38498.1 GI:986977	
VERSION	L38498.1	GI:986977	
KEYWORDS	ccdB gene; cloning vector; kanamycin resistance.		
SOURCE	Cloning vector pKIL18		
ORGANISM	Cloning vector pKIL18		
REFERENCE	1 (bases 1 to 2999)		
AUTHORS	Bernard, P.		
TITLE	New ccdB positive-selection cloning vectors with kanamycin or chloramphenicol selectable markers		
JOURNAL	Gene 162 (1), 159-160 (1995)		
MEDLINE	96009896		
PUBMED	7557407		
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		Best Local Similarity 93.4%; Pred. No. 0;	
		Matches 2388; Conservative 0; Mismatches 26; Indels 144; Gaps 1;	
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Db	2699	GTTTATCCACAGATCAGGGGATTAACCGAGGAAGACATGTGAGCAAAAGGCCAGCAAA	2640
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ORGANISM Cloning vector pKIL119  
 REFERENCE artificial sequences; vectors.  
 1 (bases 1 to 2999)  
 AUTHORS Bernard, P.  
 TITLE New ccdB positive-selection cloning vectors with kanamycin or chloramphenicol selectable markers  
 JOURNAL Gene 162 (1), 159-160 (1995)  
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 PUBMED 7557407  
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VERSION AY189829.1 GI:28435539  
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SOURCE his-3 integration vector pJHAM004  
ORGANISM his-3 integration vector pJHAM004  
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AUTHORS Lee,D.W., Haag,J.R. and Aramayo,R.  
TITLE Construction of strains for rapid homokaryon purification after integration of constructs at the histidine-3 (his-3) locus of Neurospora crassa  
JOURNAL Curr. Genet. 43 (1), 17-23 (2003)  
PUBMED 1264841  
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AUTHORS Lee,D.W., Haag,J.R. and Aramayo,R.  
TITLE Direct Submission  
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JOURNAL	J. Biotechnol. 104 (1-3), 287-299 (2003)	
MEDLINE	22830032	
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AUTHORS Kirchner,O. and Tauch,A.
TITLE Tools for genetic engineering in the amino acid-producing bacterium
Corynebacterium glutamicum
JOURNAL J Biotechnol. 104 (1-3), 287-299 (2003)
MEDLINE 22830032
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 ACCESSION AV219861  
 VERSION AV219861.1 GI:29164983



KEYWORDS Shuttle vector pEC-K19MECA2  
SOURCE Shuttle vector pEC-K19MECA2  
ORGANISM artificial sequences; vectors.  
REFERENCE 1 (bases 1 to 5869)  
AUTHORS Kirchner,O. and Tauch,A.  
TITLE Tools for genetic engineering in the amino acid-producing bacterium  
Corynebacterium glutamicum  
J. Biotechnol. 104 (1-3), 287-299 (2003)  
MEDLINE 22830032  
PUBMED 12948646  
REFERENCE 2 (bases 1 to 5869)  
AUTHORS Kirchner,O. and Tauch,A.  
TITLE Direct Submission  
JOURNAL Submitted (15-JAN-2003) Department of Genetics, University of  
Bielefeld, Universitaetsstrasse 25, Bielefeld D-33615, Germany  
LOCATION/Qualifiers  
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Db	3857	GGTCTCTTGTGCTGCTTTCGAACCCAGAGTCCCGCTCAGAGAACTCGTCAAGAAG	3798	Db	2777	GTAGCTGACATTCATCCGCGGCTCAGCACCGTTTCTCGGACTGGCTTCTACGTGTTCGG	2718
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Db	3377	ATGAGCCATGATGATATTTCTCGGAGGAGCAAGGTGAGTACAGAGATCTCGGCC	3318	PUBMED	22830032		
Qy	4640	CGGCATTCGCCCCAATAGCAGCAGTCCCTTCGCGCTTCAGTGACAAAGTCCGAGCAGC	4699	REFERENCE	3 (bases 1 to 3035)		
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Qy	4700	TGCGCAAGGAACGCCGCTGCTGGCGAGCCAGATAGCCGCGTGCCTGCTCGAGTTC	4759	TITLE	Direct Submission		
Db	3257	TGCGCAAGGAACGCCGCTGCTGGCGAGCCAGATAGCCGCGTGCCTGCTCGAGTTC	3198	JOURNAL	Submitted (22-JAN-2003) Department of Genetics, University of		
Qy	4760	ATTGAGGACCGGACAGTGGTCTTCACAAAAGAACCGGCGCCCTCGCTGTCAGAG	4819	MEDLINE	Bielefeld, Universitaetsstrasse 25, Bielefeld D-33615, Germany		
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QY	3381	CGAACCCCGTTTCAGCCGACCGCTCGCTTATCCGGTAACTATCTGTTGAGTCCAA 3440
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QY	3441	CCCGGTAAGACACGACTTATCGCATTCGGCAGCAGCCACTGGTAACAGGATTAGCAGGC 3500
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QY	3501	GAGGTATGTAGGCGGTGCTACAGATTCTTGAAATGGTGGCCCTAACTACGGCTACACTAG 3560
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QY	4019	-----CGGCGTCCCGAAAAACGATTCCGAAAGCCCAA 4049
Db	1527	GGCGTCTGGACTATGAGCACGTCGCGAGGGCGTCCCGAAAAACGATTCCGAAAGCCCAA 1468
QY	4050	CTTTTCATAGAGCGCGGCTGGATCGAATCTCGTGTATGGCAGGTTGGCGCTCGGTTG 4109
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QY	4110	GTGCGTCATTTCGAAACCCAGAGTCCCGCTCAGAGAACTCGTCAAGAACGCGCATAG 4169
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QY	4170	GCATGCGCTCGGAATCGGAGCGGGATACCGTAAAGACAGAGGAGCGGTACAGCCCAT 4229
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QY	4230	TCGCCGCCAGCTTTCAGCAATATCAGGGTAGCCAAACGCTATGCTCTGATAGCGTCC 4289
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QY	4290	GCCACACCCAGCGCGCACAGTCGATGAATCCAGAAAAAGCGCATTTTCCACCATGATA 4349
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QY	4350	TTCCGCAAGCAGGCATTCGCCATGGGTACAGACAGATCCTCGCGCTCGGCGATCGCGCC 4409
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QY	4410	TTGAGCCTGGCGAAGCAGTTGGCTGGCGAGCCCTGATGCTCTTCGTCAGATCATCC	4469	AUTHORS	Tauch, A., Kirchner, O., Löffler, B., Gotker, S., Puhler, A. and
Db	1107	TTGAGCCTGGCGAAGCAGTTGGCTGGCGAGCCCTGATGCTCTTCGTCAGATCATCC	1048	TITLE	Kalinowski, J.
QY	4470	TGATCGACAAGACCGGCTTCATCCGAGTACGTCGCTCGATGCGATGTTTCGTTGG	4529	JOURNAL	Curr. Microbiol. 45 (5), 362-367 (2002)
Db	1047	TGATCGACAAGACCGGCTTCATCCGAGTACGTCGCTCGATGCGATGTTTCGTTGG	988	MEDLINE	22217619
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Db	987	TGATCGACAAGACCGGCTTCATCCGAGTACGTCGCTCGATGCGATGTTTCGTTGG	928	REFERENCE	2 (bases 1 to 3053)
QY	4590	ATGGATACCTTTTCGCGACGAGCAAGGTGAGATGACAGGAGATCCTGCCCGGCACTTCG	4649	AUTHORS	Tauch, A., Kirchner, O., Löffler, B., Gotker, S., Puhler, A. and
Db	927	ATGGATACCTTTTCGCGACGAGCAAGGTGAGATGACAGGAGATCCTGCCCGGCACTTCG	868	TITLE	Kalinowski, J.
QY	4650	CCCAATAGCAGCAGTCCCTTCCGCTTTCAGTGACAACGTCGAGCAGCTGGCGAAGGA	4709	JOURNAL	Direct Submission
Db	867	CCCAATAGCAGCAGTCCCTTCCGCTTTCAGTGACAACGTCGAGCAGCTGGCGAAGGA	808	Submitted (22-JAN-2003)	Department of Genetics, University of
QY	4710	ACGCCGCTGGTGGCAGCAGTACGCGCTGCTCGCTCGCTGCTGCTGCTGCTGCTGCT	4769	Bielefeld, Universitaetsstrasse 25, Bielefeld D-33615, Germany	
Db	807	ACGCCGCTGGTGGCAGCAGTACGCGCTGCTCGCTCGCTGCTGCTGCTGCTGCTGCT	748	FEATURES	
QY	4770	CGGACAGGTCGCTTTCGACAAGAAACCGGCGCCCTCGCTGCTGCTGCTGCTGCTGCT	4829	source	1. .3053
Db	747	CGGACAGGTCGCTTTCGACAAGAAACCGGCGCCCTCGCTGCTGCTGCTGCTGCTGCT	688	gene	/organism="Cloning vector pK18PolyF2"
QY	4830	CGGACATCAGCAGCAGTGTGCTGTTGTCGCGAGTCATGCGGATAGCTTCCACC	4889	CDS	/mol_type="genomic DNA"
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QY	4890	CAAGCGCGGAGAACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT	4949		/lab_host="Escherichia coli"
Db	627	CAAGCGCGGAGAACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT	568		602. .1396
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Db	567	CTGTCTCTTGATCAGATCTTGATCTCCCTGCGCATCAGATCTTGGCGGCAAGAGCC	508		/genes="aph(3')-IIa"
QY	5010	ATCCAGTTTACTTTCGAGGCTTCCCACTTACAGAGGCGCGCCGAGTGGCAATTC	5069		/note="aminoglycoside phosphotransferase"
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QY	5250	CAGCCCTTGGCCTGAGTGTGCTTGGCGAGCGTG 5283			EHGLAPAEFLPARKARMPDGLVTHGDACLPIWVNGRFSGFIDCGRLGVADRY
Db	267	CAGCCCTTGGCCTGAGTGTGCTTGGCGAGCGTG 234			QDIALATRIAEELGGEWDRFLVLVGLIAPDSQRTAFYELLDEFF"
RESULT 15					
LOCUS	AY222811/c				
DEFINITION	Cloning vector pK18PolyF2, complete sequence.				
ACCESSION	AY222811				
VERSION	AY222811.1				
KEYWORDS	Cloning vector pK18PolyF2				
SOURCE	Cloning vector pK18PolyF2				
ORGANISM	artificial sequences; vectors.				
REFERENCE	1 (bases 1 to 3053)				

QY	2721	GTCTAGCTGTTTCTGCTGTAATTTGTTATCCGCTCACAAATCCACACATACACGAC	2780	Query Match	39.3%; Score 2078; DB 12; Length 3053;
Db	3045	GTCTAGCTGTTTCTGCTGTAATTTGTTATCCGCTCACAAATCCACACATACACGAC	2986	Best Local Similarity	86.7%; Pred. No. 0;
QY	2781	CGGAAGCATAAAGTGAAGCTGGGTCCTTAATGATGAGTGAATCACTCACTTAATTCG	2840	Matches 2423; Conservative	0; Mismatches 140; Indels 231; Gaps 3;
Db	2985	CGGAAGCATAAAGTGAAGCTGGGTCCTTAATGATGAGTGAATCACTCACTTAATTCG	2926		
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Db	2865	CGGCAACGCGCGGAGAGCGGTTTCGGTATTTGGGCGCTCTTCGCTTCCTCGCTCAC	2806		
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Db	2805	TGACTCGCTGCGCTCGGTCGTTTCGGCTCGGCGAGCGGTATCAGTCACTCAAAAGCGGT	2746		
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Db	2745	AATACGGTTATCCAGAAATCAGGGGATACCGCAGGAAGACATGTGAGCAAAAGGCCA	2686		
QY	3081	GCAAAAGGCCAGAACCCGTAAGGCGCGTGTGCTGGCGTTTTCCTAGGCTCGCC	3140		
Db	2685	GCAAAAGGCCAGAACCCGTAAGGCGCGTGTGCTGGCGTTTTCCTAGGCTCGCC	2626		





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Db 465 GGTTCGCTTGCTGTCATATAAACCGCCAGTCTAGCTATCGCCATGTAAGCCCACTGCAA 406
QY 5130 GCTACCTGCTTCTCTCTTTGCGCTTGGCTTTTCCCTTGTCCAGATAGCCCAAGTAGCTGACA 5189
Db 405 GCTACCTGCTTCTCTCTTTGCGCTTGGCTTTTCCCTTGTCCAGATAGCCCAAGTAGCTGACA 346
QY 5190 TTCATCCGGGGTCAGACCCGTTTCTGCGGACTGGCTTTCTACGTGTTCGGCTTCCTTTAG 5249
Db 345 TTCATCCGGGGTCAGACCCGTTTCTGCGGACTGGCTTTCTACGTGTTCGGCTTCCTTTAG 286
QY 5250 CAGCCCTTGGCCCTGAGTGTGCTGCGGACGCGTG 5283
Db 285 CAGCCCTTGGCCCTGAGTGTGCTGCGGACGCGTG 252
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Search completed: August 4, 2004, 11:02:29  
Job time : 19782 secs

GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: August 4, 2004, 01:48:34 ; Search time 1848 Seconds  
(without alignments)

12144.605 Million cell updates/sec

Title: US-09-921-143-36

Perfect score: 5283

Sequence: 1 aagcttgacattatgcgact.....tgagtgttcgcgcagcgtg 5283

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 3373863 segs, 2124099041 residues

Total number of hits satisfying chosen parameters: 6747726

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : N\_Geneseq\_29Jan04.\*

- 1: Geneseqn1980s.\*
- 2: Geneseqn1990s.\*
- 3: Geneseqn2000s.\*
- 4: Geneseqn2001as.\*
- 5: Geneseqn2001bs.\*
- 6: Geneseqn2002s.\*
- 7: Geneseqn2003as.\*
- 8: Geneseqn2003bs.\*
- 9: Geneseqn2003cs.\*
- 10: Geneseqn2004s.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	5283	100.0	5283	6	ABK10062 Expressio
2	2240	42.4	8349	3	AA15565 pMON30464
3	2017.2	38.2	6136	2	AAV29673 Hybrid NA
C 4	1793.4	33.9	4800	2	AAV52020 Synthetic
C 5	1652.4	31.3	5594	2	AAV33629 GNSA 981
C 6	1634.4	30.9	5285	4	AAH74865 Nucleotid
C 7	1632.8	30.9	5285	7	ABX94355 Rolling c
C 8	1618.2	30.6	6561	2	AAV33630 Plasmid V
9	1603.8	30.4	2192	6	ABQ78294 Nucleotid
10	1603.8	30.4	3534	6	ABQ78293 Nucleotid
11	1603.8	30.4	3534	8	AA162060 TV-GHRH p
12	1603.8	30.4	3534	8	AA162062 Wild-type
13	1603.8	30.4	3534	8	AA162059 TI-GHRH p
14	1603.8	30.4	3534	8	AA162058 pSP-HV-GH
15	1603.8	30.4	3534	8	AA162061 15/27/28-
16	1603.8	30.4	3534	8	AA160444 TI-GHRH p
17	1603.8	30.4	3534	8	AA160445 TV-GHRH p
18	1603.8	30.4	3534	8	AA160446 15/27/28
19	1603.8	30.4	3534	8	AA160443 pSP-HV-GH
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22	1603.8	30.4	3534	9	ACF04660 15/27/28
23	1603.8	30.4	3534	9	ACF04657 HV-GHRH o

24	1603.8	30.4	3534	9	ACF04659
25	1603.8	30.4	3534	9	ACF04658
26	1603.8	30.4	3599	2	AAV50428
27	1603.8	30.4	3599	2	AAV40796
28	1603.4	30.4	3558	8	AA160457
29	1602.2	30.3	3600	2	AAV50427
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31	1602.2	30.3	5707	2	AAV88055
32	1600	30.3	5966	2	AAZ40417
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C 34	1570.8	29.7	5068	2	AAH84027
35	1570	29.7	4517	5	AAH24427
36	1570	29.7	4518	2	AAV33626
C 37	1570	29.7	4775	8	ACC84214
C 38	1570	29.7	4886	6	AAH42469
C 39	1570	29.7	4886	7	ACA61962
C 40	1570	29.7	5031	2	AAZ25355
C 41	1570	29.7	5054	2	AAZ25354
C 42	1570	29.7	5130	2	AAZ25353
C 43	1570	29.7	5168	2	AAZ25351
C 44	1570	29.7	5619	3	AAA07773
C 45	1570	29.7	5627	3	AAA07778

## ALIGNMENTS

RESULT 1  
ABK10062  
ID ABK10062 standard; DNA; 5283 BP.  
XX  
AC ABK10062;  
XX  
DT 21-MAY-2002 (first entry)  
XX  
DE Expression vector construct pVGI.1 containing VEGF-2 insert.  
XX  
KW Human; vascular endothelial growth factor 2; VEGF-2; ds; pVGI.1;  
KW chronic limb ischaemia; myocardial ischaemia; autoimmune disorder; pHE4a;  
KW allergic reaction; organ rejection; inflammatory condition; arrhythmia;  
KW hyperproliferative disorder; viral infection; bacterial infection;  
KW fungal infection; parasitic infection; cardiovascular disorder; embolism;  
KW heart valve disease; aneurysm; arterial occlusive disorder; gene therapy.  
XX  
OS Synthetic.  
XX  
DN WO200211769-A1.  
XX  
PD 14-FEB-2002.  
XX  
PF 03-AUG-2001; 2001WO-US024658.  
XX  
PR 04-AUG-2000; 2000US-0223276P.  
XX  
PA (HUMA-) HUMAN GENOME SCI INC.  
XX  
PI Coleman TA;  
XX  
XX WPI; 2002-217153/27.  
XX  
DR Isolated nucleic acid having expression vector construct with vascular  
XX endothelial growth factor-2 insert, useful for treating chronic limb  
XX ischemia or myocardial ischemia, autoimmune disorders and allergic  
XX conditions.  
XX  
PS Disclosure; Fig 31; 241pp; English.  
XX  
CC The invention relates to an isolated nucleic acid comprising pVGI.1  
XX expression vector construct containing the vascular endothelial growth  
XX factor 2 (VEGF-2) insert. The nucleic acid is useful for producing a host  
XX cell by transducing, transforming or transfecting a host cell with the  
XX DNA and for treating a patient having chronic limb ischaemia or  
XX myocardial ischaemia, or a disease or disorder selected from autoimmune

CC disorders (e.g. rheumatoid arthritis, dermatitis), allergic reactions or  
CC conditions (e.g. asthma), organ rejection, inflammatory conditions (e.g.  
CC Crohn's disease), hyperproliferative disorders (e.g. Gaucher's disease),  
CC diseases due to viral, bacterial, fungal or parasitic infection,  
CC cardiovascular disorders (e.g. cardiomyopathy), arrhythmia, heart valve  
CC diseases, aneurysms, arterial occlusive disorders and embolism. This  
CC sequence represents the pVGI.1 expression vector containing the VEGF-2  
CC insert  
XX  
SQ Sequence 5283 BP; 1244 A; 1422 C; 1417 G; 1200 T; 0 U; 0 Other;  
Query Match 100.0%; Score 5283; DB 6; Length 5283;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 5283; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 AAGCTTGACCTTATCGGACTTTCCTACTTGGCAGTACATCTACGTATTAGTCATCGCTAT 60  
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DB 61 TACCATGGTGATGCGGTTTGGCAGTACATCAATGGCGGTGATAGCGGTTTGACTCAG 120  
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DB 121 GGGATTCCAGTCTCCACCCCACTGAGTCAATGGAGTTTGTGTCACCAAAATCA 180  
QY 181 ACGAGACTTTCAAAATGCTGTAACAACCTCGCCCACTGACGCAAAATGGCGGTAGGCG 240  
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DB 301 CATGCGGATGTTGGGAGTAAGTGATGATGCTGGTATGATGCTGCTGTAGGAAG 360  
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QY 421 GTATTAAAGTCCAGCTCGATCAATAAAGCGCATTTGACCATTCACCACTTGTGTG 480  
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QY 541 CTGCTGCGGCTGCGCTGCTCCGGGTCTTCGCGAGCGCGCGCGCGCGCGCTTC 600  
DB 541 CTGCTGCGGCTGCGCTGCTCCGGGTCTTCGCGAGCGCGCGCGCGCGCGCTTC 600  
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DB 1381 TGTGCTGAGAGCGGGCTTCGGCTGCGAGTGTGACCAACCAACCAAGAGCTGAGTACAG 1440  
QY 1441 AACTCATGCGAGTGTCTGTAACCAACCAACCTTCCCAGCAATGTGGGCGCAACCGA 1500  
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QY 1801 AGCACCTTTGTTGTTCTTCACTTGGTGAAGCTCTCTACCTGTTGTTGTTGTTGTTGAT 1860  
DB 1801 AGCACCTTTGTTGTTCTTCACTTGGTGAAGCTCTCTACCTGTTGTTGTTGTTGTTGAT 1860  
QY 1861 TCTTCTACACACCATGTCCCGCGGAAAGTGGAGACCCACAAAGTAAAGTCTGCTCT 1920  
DB 1861 TCTTCTACACACCATGTCCCGCGGAAAGTGGAGACCCACAAAGTAAAGTCTGCTCT 1920  
QY 1921 GAATTCATCCCAAGTCTAACTACCTGTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT 1980  
DB 1921 GAATTCATCCCAAGTCTAACTACCTGTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT 1980



[illegible]

Db	6031	ACTACATTAATTCGCTGCGCTCACTGCCCGCTTTCCAGTCGGGAACCTGTCGTGCCA	6090	7025	-----TT	7026
QY	2886	GCTGCATTAATGAATCGGCAACGCGCGGGAGAGCGGTTTTCGCTATTTGGGCGCTCTTC	2945	3966	GGGTTGGGCGAAGAACTCCAGCATGAGATCCCGCGCTGGAGGATCATCCAGCGCGTC	4025
Db	6091	GCTGCATTAATGAATCGGCAACGCGCGGGAGAGCGGTTTTCGCTATTTGGGCGCTCTTC	6150	7027	GGGTTGGGCGAAGAACTCCAGCATGAGATCCCGCGCTGGAGGATCATCCAGCGCGTC	7086
QY	2946	CGCTTCTCGCTCACTGACTCGCTGCGCTGCGTTCGCTTCGCTTCGCGCGAGCGGTATCAGC	3005	4026	CCGGAAGAACGATTCGGAAGCCCAACTTTTCATAGAGGGCGGCTGGAAATCGAAATCTCG	4085
Db	6151	CGCTTCTCGCTCACTGACTCGCTGCGCTGCGTTCGCTTCGCTTCGCGCGAGCGGTATCAGC	6210	7087	CCGGAAGAACGATTCGGAAGCCCAACTTTTCATAGAGGGCGGCTGGAAATCGAAATCTCG	7146
QY	3006	TCACCTCAAGAGCGGTAAATACGGTTATCCACAGATCAGGGGATACGCGAGGAAGAAAT	3065	4086	TGATGCGAGGTTGGCGTCGCTTCGCTTCGCTTCGCTTCGCTTCGCTTCGCTTCGCTTCGCT	4145
Db	6211	TCACCTCAAGAGCGGTAAATACGGTTATCCACAGATCAGGGGATACGCGAGGAAGAAAT	6270	7147	TGATGCGAGGTTGGCGTCGCTTCGCTTCGCTTCGCTTCGCTTCGCTTCGCTTCGCTTCGCT	7206
QY	3066	GTGACGAAAGCCAGCAGCAAGGCGCAGGAACCGTAAAGGCGCGCTTCGCTGGCGTTTTT	3125	4146	AACTCGTCAAGAGCGGTAGAGCGGATGAGAGCGGATGCGCTTCGCTTCGCTTCGCTTCGCT	4205
Db	6271	GTGACGAAAGCCAGCAGCAAGGCGCAGGAACCGTAAAGGCGCGCTTCGCTGGCGTTTTT	6330	7207	AACTCGTCAAGAGCGGTAGAGCGGATGAGAGCGGATGCGCTTCGCTTCGCTTCGCTTCGCT	7266
QY	3126	CCATAGGCTCCGCGCCCTGACGAGCATCAAAATAATCGACGCTCAAGTCAGAGTGCGC	3185	4206	AGCAGAGAAAGCGGTAGAGCGGATGAGAGCGGATGCGCTTCGCTTCGCTTCGCTTCGCT	4265
Db	6331	CCATAGGCTCCGCGCCCTGACGAGCATCAAAATAATCGACGCTCAAGTCAGAGTGCGC	6390	7267	AGCAGAGAAAGCGGTAGAGCGGATGAGAGCGGATGCGCTTCGCTTCGCTTCGCTTCGCT	7326
QY	3186	AAACCCGACAGGACTATAAAGATACAGGCGTTTCCCGCTGGAAGCTCCCTCGTGGCTC	3245	4266	AAACGCTATGCTGATAGCGGTCCGCGCACACCCAGCGCGGCGCACAGTCGATGAATCCAGAA	4325
Db	6391	AAACCCGACAGGACTATAAAGATACAGGCGTTTCCCGCTGGAAGCTCCCTCGTGGCTC	6450	7327	AAACGCTATGCTGATAGCGGTCCGCGCACACCCAGCGCGGCGCACAGTCGATGAATCCAGAA	7386
QY	3246	TCCTGTTCCGACCCCTGCGGCTTACGGATACCTGTCGCGCTTTCTCCCTCGGGAAGCGT	3305	4326	AAGCGGCGCATTTTCCACCATGATATTCGGGAAGCAGGATCGCATTCGATGAATCCAGAA	4385
Db	6451	TCCTGTTCCGACCCCTGCGGCTTACGGATACCTGTCGCGCTTTCTCCCTCGGGAAGCGT	6510	7387	AAGCGGCGCATTTTCCACCATGATATTCGGGAAGCAGGATCGCATTCGATGAATCCAGAA	7446
QY	3306	GGCGCTTCTCATAGCTACAGCTGAGGTATCTCAGTTCGGTTCGCTTCGCTTCGCTTCGCT	3365	4386	TCCTCGCGCTCGCGCATTCGCGCGCTTCGCGCGCTTCGCGCGCTTCGCGCGCTTCGCGCGCT	4445
Db	6511	GGCGCTTCTCATAGCTACAGCTGAGGTATCTCAGTTCGGTTCGCTTCGCTTCGCTTCGCT	6570	7447	TCCTCGCGCTCGCGCATTCGCGCGCTTCGCGCGCTTCGCGCGCTTCGCGCGCTTCGCGCGCT	7506
QY	3366	GCTGGGCTGTGTGACGAACCCCGCTTACGCCGACCGCTGCGCTTATCCCGTAACTA	3425	4446	TGATGCTTCTGCTCCAGATCATCTGATCGAACAGCGGCTTCATCCCGAGTACGTGCT	4505
Db	6571	GCTGGGCTGTGTGACGAACCCCGCTTACGCCGACCGCTGCGCTTATCCCGTAACTA	6630	7507	TGATGCTTCTGCTCCAGATCATCTGATCGAACAGCGGCTTCATCCCGAGTACGTGCT	7566
QY	3426	TCGCTTTGAGTCCMACCCGCTAAGACACGACTTATCGCCACTGGCAGCAGCACTGCTAA	3485	4506	CGCTCGATCGATGTTTCGCTTCGCTTCGCTTCGCTTCGCTTCGCTTCGCTTCGCTTCGCT	4565
Db	6631	TCGCTTTGAGTCCMACCCGCTAAGACACGACTTATCGCCACTGGCAGCAGCACTGCTAA	6690	7567	CGCTCGATCGATGTTTCGCTTCGCTTCGCTTCGCTTCGCTTCGCTTCGCTTCGCTTCGCT	7626
QY	3486	CAGGATTAGCAGAGCGAGTATGAGCGGTGCTACAGAGTTCTTGAAGTGGTGGCTTAA	3545	4566	AGCGCGCGCATTCGATCAGCCATGATGATGATGATGATGATGATGATGATGATGATGATGAT	4625
Db	6691	CAGGATTAGCAGAGCGAGTATGAGCGGTGCTACAGAGTTCTTGAAGTGGTGGCTTAA	6750	7627	AGCGCGCGCATTCGATCAGCCATGATGATGATGATGATGATGATGATGATGATGATGATGAT	7686
QY	3546	CTACGGCTACACTAGAGAACAGTATTTGGTATCTGGCTCTGCTGAAGCCAGTTACCTT	3605	4626	AGGAGATTCCTGCGCGCGCATTCGCGCATTCGCGCATTCGCGCATTCGCGCATTCGCGCAT	4685
Db	6751	CTACGGCTACACTAGAGAACAGTATTTGGTATCTGGCTCTGCTGAAGCCAGTTACCTT	6810	7687	AGGAGATTCCTGCGCGCGCATTCGCGCATTCGCGCATTCGCGCATTCGCGCATTCGCGCAT	7746
QY	3606	CGGAAAAAGAGTTGGTACGCTTCGCTTCGCTTCGCTTCGCTTCGCTTCGCTTCGCTTCGCT	3665	4686	ACGTCGAGCAGCTGGCGAAGAAACGCGCTCGTGGCGAGCAAGCATAGCCCGCTGCTG	4745
Db	6811	CGGAAAAAGAGTTGGTACGCTTCGCTTCGCTTCGCTTCGCTTCGCTTCGCTTCGCTTCGCT	6870	7747	ACGTCGAGCAGCTGGCGAAGAAACGCGCTCGTGGCGAGCAAGCATAGCCCGCTGCTG	7806
QY	3666	TTTTTTTCAAGCAGCAGATTCGCGCAGAAAAAAGAGTCTCAAGAGATCCTTTGAT	3725	4746	TCGCTCTGAGTTCATTCAGGGCACCGGACAGCTCGCTTCGCTTCGCTTCGCTTCGCTTCGCT	4805
Db	6871	TTTTTTTCAAGCAGCAGATTCGCGCAGAAAAAAGAGTCTCAAGAGATCCTTTGAT	6930	7807	TCGCTCTGAGTTCATTCAGGGCACCGGACAGCTCGCTTCGCTTCGCTTCGCTTCGCTTCGCT	7866
QY	3726	CTTTTCTACGGGTCTGACGCTCAGTGGAGCAAACTCAGCTTAAAGGATTTTGGTTCAT	3785	4806	CCCTGCGCTTGACAGCGGAAACACCGCGGATCAGAGCAGCGGATTCGCTTCGCTTCGCTTCGCT	4865
Db	6931	CTTTTCTACGGGTCTGACGCTCAGTGGAGCAAACTCAGCTTAAAGGATTTTGGTTCAT	6990	7867	CCCTGCGCTTGACAGCGGAAACACCGCGGATCAGAGCAGCGGATTCGCTTCGCTTCGCTTCGCT	7926
QY	3786	GAGATTATCGTACCAAGCGGCGATTCGCTTCGCTTCGCTTCGCTTCGCTTCGCTTCGCTTCGCT	3845	4866	TCATAGCCCAATAGCTTCACCCAGCGGCGGAGAACCTTCGCTTCGCTTCGCTTCGCTTCGCT	4925
Db	6991	GAGATTATCGTACCAAGCGGCGATTCGCTTCGCTTCGCTTCGCTTCGCTTCGCTTCGCTTCGCT	7024	7927	TCATAGCCCAATAGCTTCACCCAGCGGCGGAGAACCTTCGCTTCGCTTCGCTTCGCTTCGCT	7986
QY	3846	GATGCGCGGATAGCGCTGCTGCTTCTCGGATGCGCGGATTTGCACTGCGCGGTAGAA	3905	4926	TCAATCATGCGAAACGATCCTCATCTGCTTCGCTTCGCTTCGCTTCGCTTCGCTTCGCTTCGCT	4985
Db	7025	-----	7024	7987	TCAATCATGCGAAACGATCCTCATCTGCTTCGCTTCGCTTCGCTTCGCTTCGCTTCGCTTCGCT	8046
QY	3906	CTCCGCGAGTCTGTCAGGCTCAGGCGAGCTGAAACCACTCGGAGGGATCGAGCCC	3965	4986	CAGATCTTGGCGGCAAGAAACGATCCTCATCTGCTTCGCTTCGCTTCGCTTCGCTTCGCTTCGCT	5045
				8047	CAGATCTTGGCGGCAAGAAACGATCCTCATCTGCTTCGCTTCGCTTCGCTTCGCTTCGCTTCGCT	8106





Db 3445 ----- 3446  
QY 3964 CCGGGTGGGGAAGAACTCCAGCATGATATCCCGCGCTGGAGGATCATCCAGCCGGCG 4023  
Db 3445 TTGGGTGGGGAAGAACTCCAGCATGATATCCCGCGCTGGAGGATCATCCAGCCGGCG 3386  
QY 4024 TCCCGGAAACGATTCGGAAGCCCAACCTTTCATAGAGGGCGGCGGTGGAATCGAAATCT 4083  
Db 3385 TCCCGGAAACGATTCGGAAGCCCAACCTTTCATAGAGGGCGGCGGTGGAATCGAAATCT 3326  
QY 4084 CGTGATGCGAGGTTGGGCGTCCGTTGCTCGTTCGATTCGGAACCCAGAGTCCCGCTCAGA 4143  
Db 3325 CGTGATGCGAGGTTGGGCGTCCGTTGCTCGTTCGATTCGGAACCCAGAGTCCCGCTCAGA 3266  
QY 4144 AGAATCTCTAAGAGGCGATAGAGGCGATCGCTGCGAATTCGGAGCGGCGATACCGT 4203  
Db 3265 AGAATCTCTAAGAGGCGATAGAGGCGATCGCTGCGAATTCGGAGCGGCGATACCGT 3206  
QY 4204 AAAGCAGGAGGAGGCTCAGCCCAATTCGCGCGCAAGCTTTCAGCAATATCACGGCTAG 4263  
Db 3205 AAAGCAGGAGGAGGCTCAGCCCAATTCGCGCGCAAGCTTTCAGCAATATCACGGCTAG 3146  
QY 4264 CCAACGCTATGCTCTGATAGCGGTCCGCCACACCCAGCGCCACAGTTCGATGATCCAG 4323  
Db 3145 CCAACGCTATGCTCTGATAGCGGTCCGCCACACCCAGCGCCACAGTTCGATGATCCAG 3086  
QY 4324 AAAAGCGGCAATTTCCACCATGATATTTCGCAAGCAGGATCGCCATCGGTTCACGACGA 4383  
Db 3085 AAAAGCGGCAATTTCCACCATGATATTTCGCAAGCAGGATCGCCATCGGTTCACGACGA 3026  
QY 4384 GATCTCGCGTCGGCATCGCGCTTGAGCTTGCGGCAACAGTTCGCTGGCGCGAGCC 4443  
Db 3025 GATCTCGCGTCGGCATCGCGCTTGAGCTTGCGGCAACAGTTCGCTGGCGCGAGCC 2966  
QY 4444 CCTGATGCTCTTCGTCAGATCATCTCTGATCGCAACAGACCGCTTCATCCGAGTAGCTG 4503  
Db 2965 CCTGATGCTCTTCGTCAGATCATCTCTGATCGCAACAGACCGCTTCATCCGAGTAGCTG 2906  
QY 4504 CTGCTCGATGCGATGTTTCGTTGTTGTCGATGCGGCGAGTAGCCGATCAAGCGTAT 4563  
Db 2905 CTGCTCGATGCGATGTTTCGTTGTTGTCGATGCGGCGAGTAGCCGATCAAGCGTAT 2846  
QY 4564 GCAGCCGCGCATTCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 4623  
Db 2845 GCAGCCGCGCATTCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2786  
QY 4624 ACAGGAGATCCTGCCCGGCACTTCGCCCAATAGCAGCCAGTCCCTTCGCGTTCAGTGA 4683  
Db 2785 ACAGGAGATCCTGCCCGGCACTTCGCCCAATAGCAGCCAGTCCCTTCGCGTTCAGTGA 2726  
QY 4684 CAACGTCGAGCAGCTGCGCAAGAACGCCGCTCGTGGCCAGCCAGTAGCCGCGCTG 4743  
Db 2725 CAACGTCGAGCAGCTGCGCAAGAACGCCGCTCGTGGCCAGCCAGTAGCCGCGCTG 2666  
QY 4744 CTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 4803  
Db 2665 CTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2606  
QY 4804 GCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 4863  
Db 2605 GCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2546  
QY 4864 AGTCATAGCCGAATAGCTCTCCACCAAGCGCGCCGAGAACCTGCTGCTGCTGCTGCTGCTGCT 4923  
Db 2545 AGTCATAGCCGAATAGCTCTCCACCAAGCGCGCCGAGAACCTGCTGCTGCTGCTGCTGCTGCT 2486  
QY 4924 GTTCATATGCGAAGCATCTCATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 4983  
Db 2485 GTTCATATGCGAAGCATCTCATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2426  
QY 4984 ATCAGATCTCTGGCGCAAGAACCATCCAGTTTACCTTTTTCAGGCTTCCCAACCTTAC 5043

Db 2425 ATCAGATCTTTGGCGGCAAGAAAGCCATCCAGTTTACTTTGCGAGGCTTCCCAACCTTAC 2366  
QY 5044 CAGAGGGCGCCCGCAGCTGGCAATTCGGTTTGGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCT 5103  
Db 2365 CAGAGGGCGCCCGCAGCTGGCAATTCGGTTTGGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2306  
QY 5104 GCTATCGCCATGTAAAGCCACTGCAAGCTACTGCTTCTCTTTGCGGCTTGGGTTTCC 5163  
Db 2305 GCTATCGCCATGTAAAGCCACTGCAAGCTACTGCTTCTCTTTGCGGCTTGGGTTTCC 2246  
QY 5164 TTGTCAGATAGCCAGTAGCTGATCATTCATCCGGGTCAGCACCGTTTCTTGGGACTGG 5223  
Db 2245 TTGTCAGATAGCCAGTAGCTGATCATTCATCCGGGTCAGCACCGTTTCTTGGGACTGG 2186  
QY 5224 CTTTCTAGGTTTCGGCTTCTTTAGCAGCCCTTTCGGCCCTGAGTGTGTCGGGAGCGTG 5283  
Db 2185 CTTTCTAGGTTTCGGCTTCTTTAGCAGCCCTTTCGGCCCTGAGTGTGTCGGGAGCGTG 2126

## RESULT 4

AAX52020/c

ID AAX52020 standard; DNA; 4800 BP.

XX AC AAX52020;

XX AC AAX52020;

XX DT 18-JUN-1999 (first entry)

XX XX Synthetic DNA plasmid sequence synlux4.

XX XX DNA plasmid; lux A; lux B; Vibrio fischeri; luciferase; promoter;

XX KW tn9 kanamycin/neomycin phosphotransferase; DNA synthesis;

XX KW replication competent double-stranded polynucleotide; ss.

XX OS Synthetic.

XX XX WO9914318-A1.

XX XX 25-MAR-1999.

XX PF 16-SBP-1998; 98WO-US019312.

XX XX 16-SBP-1997; 97US-0059017P.

XX PA (TEXA ) UNIV TEXAS SYSTEM.

XX XX Evans GA;

XX XX WPI; 1999-244029/20.

XX XX Synthesis of replication competent double-stranded polynucleotides.

XX XX Example 4; Fig 4A-C; 135pp; English.

XX CC The present sequence represents a synthetic DNA plasmid sequence.  
XX CC designed using synthetic parts of known plasmids. Within the sequence are  
XX CC included the sequences of lux A, lux B, the A and B components of the  
XX CC Vibrio fischeri luciferase sequence, positions of pUC19 including the  
XX CC origin of replication and replication stability sequences, and the  
XX CC promoter and coding sequence for tn9 kanamycin/neomycin  
XX CC phosphotransferase. The plasmid was synthesised form 192 50-mers (see  
XX CC AAX52021-12) to demonstrate the method of the invention. The  
XX CC specification describes a method for the synthesis of replication  
XX CC competent double-stranded polynucleotides. The method comprises  
XX CC generating a first set of oligonucleotides corresponding to the plus  
XX CC strand and a second set corresponding to the minus strand and annealing.  
XX CC The method can be used for preparing polynucleotides encoding sequences  
XX CC involved in a biochemical pathway. In particular, they can be used to  
XX CC produce polynucleotides encoding enzymes, e.g. hexokinase, phosphohexose  
XX CC isomerase, phosphofructokinase-1, aldolase, triose-phosphate isomerase,  
XX CC glyceraldehyde-3-phosphate dehydrogenase, phosphoglycerate kinase,  
XX CC phosphoglycerate mutase, enolase or pyruvate kinase. They can also be  
XX CC used for the preparation of viral particles, artificial genomes and  
XX CC artificial genetic systems

XX SQ Sequence 4800 BP; 1345 A; 1032 C; 1163 G; 1260 T; 0 U; 0 Other;  
 Query Match 33.9%; Score 1793.4; DB 2; Length 4800;  
 Best Local Similarity 91.8%; Pred. No. 3.1e-263;  
 Matches 1980; Conservative 0; Mismatches 1; Indels 176; Gaps 1;  
 3127 CATAGGCTCCGCCCCCTCAGAGCATCACAAAAATCGACGCTCAAGTCAGAGTGGCGA 3186  
 4800 CATAGGCTCCGCCCCCTCAGAGCATCACAAAAATCGAGGCTCAAGTCAGAGTGGCGA 4741  
 3187 AACCCGACAGGACTAATAAGATACAGAGGTTTCCCCCTGAGAGTCCCTCGTGGCTCT 3246  
 4740 AACCCGACAGGACTAATAAGATACAGAGGTTTCCCCCTGAGAGTCCCTCGTGGCTCT 4681  
 3247 CCGTTCGACCCCTCGGCTTACCGGATACCTGTCGCTTCTCCCTTCGGGAAGCGTG 3306  
 4680 CCGTTCGACCCCTCGGCTTACCGGATACCTGTCGCTTCTCCCTTCGGGAAGCGTG 4621  
 3307 GCGCTTCTCATAGCTCAGCTGTAGTATCTCAGTTCCGCTGAGTCCGTTCCGTTCCAAAG 3366  
 4620 GCGCTTCTCATAGCTCAGCTGTAGTATCTCAGTTCCGCTGAGTCCGTTCCGTTCCAAAG 4561  
 3367 CTGGGCTGTGGAAGAACCCCGCTTACCCGACCGCTGCGCTTATCCGTTAACTAT 3426  
 4560 CTGGGCTGTGGAAGAACCCCGCTTACCCGACCGCTGCGCTTATCCGTTAACTAT 4501  
 3427 CCGTTCGACCCCTCGGCTTACCGGATACCTGTCGCTTCTCCCTTCGGGAAGCGTG 3486  
 4500 CCGTTCGACCCCTCGGCTTACCGGATACCTGTCGCTTCTCCCTTCGGGAAGCGTG 4441  
 3487 AGGATTAGCAGAGCGAGTATGAGCGGTGTACAGAGTTCTGAGTGTGGTGGCTTAAC 3546  
 4440 AGGATTAGCAGAGCGAGTATGAGCGGTGTACAGAGTTCTGAGTGTGGTGGCTTAAC 4381  
 3547 TAGCGCTACACTAGAGAACAGTATTGGTATCTGGCTCTGCTGAGCGAGTAACTTCTC 3606  
 4380 TAGCGCTACACTAGAGAACAGTATTGGTATCTGGCTCTGCTGAGCGAGTAACTTCTC 4321  
 3607 GGAAGAAGAGTGTAGTCTTGTATCCGCAAAACAAACACCGCTGTAGCGGTGGTTTT 3666  
 4320 GGAAGAAGAGTGTAGTCTTGTATCCGCAAAACAAACACCGCTGTAGCGGTGGTTTT 4261  
 3667 TTTGTTGCAAGCAGCAGATATACCGCAGAAAAAAGAGTCTCAAGAGATCTCTTGTATC 3726  
 4260 TTTGTTGCAAGCAGCAGATATACCGCAGAAAAAAGAGTCTCAAGAGATCTCTTGTATC 4201  
 3727 TTTTCTACGGGCTGTAGCTCAGTGTGAAAGAACTCAGTTAAGGATTTTGGTCAATG 3786  
 4200 TTTTCTACGGGCTGTAGCTCAGTGTGAAAGAACTCAGTTAAGGATTTTGGTCAATG - 4142  
 3787 AGATTATCGTCGACAAAGCGGCATCTGTGCTCCCACTCTCGAGTTCCGGGGCATGG 3846  
 4141 ----- 4142  
 3847 ATGCGCGGATAGCGGTGCTGTTTCTGATGCGGACCGGATTTGCACTGCCGTAGAAC 3906  
 4141 ----- 4142  
 3907 TCCCGAGGTGCTCAGCCTCAGCAGCAGTGAACCACTCGCGAGGGATCGAGCCG 3966  
 4141 ----- GCGCG 4137  
 3967 GGGTGGCGAAGAACTCCAGCATAGATCCCGGCTGGAGATCATCAGCCGCGTCC 4026  
 4136 GGGTGGCGAAGAACTCCAGCATAGATCCCGGCTGGAGATCATCAGCCGCGTCC 4077  
 4027 CGGAAAAAGATTCGAAAGCCAACTTTTCATAGAGGCGGCTGGATCGAATCTCGT 4086  
 4076 CGGAAAAAGATTCGAAAGCCAACTTTTCATAGAGGCGGCTGGATCGAATCTCGT 4017  
 4087 GATGGCAGGTTGGCGCTGCTGTGCTGCTTTCGAAACCCACAGAGTCCCGCTCAGAGA 4146

Db QY 4016 GATGCGAGTTGGCGCTCGCTTGGTTCGATTCAGAAACCCACAGTCCCGCTCAGAGA 3957  
 4147 ACTCGTCAAGAGCGGATAGAGCGATGCGCTCGAATCGGAGCGCGGATACCGTAAA 4206  
 3956 ACTCGTCAAGAGCGGATAGAGCGGATGCGCTCGAATCGGAGCGCGGATACCGTAAA 3897  
 4207 GCACGAGAAAGCGGTACGCCCATTCGCCGCAAGCTCTTCAGCAATATACCGGGTAGCA 4266  
 3896 GCACGAGAAAGCGGTACGCCCATTCGCCGCAAGCTCTTCAGCAATATACCGGGTAGCA 3837  
 4267 ACCTATATCTGTATAGCGGTCCGCCACACCGAGCGGCGACAGTCGATGAATCCAGAAA 4326  
 3836 ACCTATATCTGTATAGCGGTCCGCCACACCGAGCGGCGACAGTCGATGAATCCAGAAA 3777  
 4327 AGCGGCAATTTCCACCATGATATTCGCAAGCAGGCTATCGCATCGGTCAGCAGAGAT 4386  
 3776 AGCGGCAATTTTCACCATGATATTCGCAAGCAGGCTATCGCATCGGTCAGCAGAGAT 3717  
 4387 CCGTCCGCTCGGCGCATGCGGCTTTGAGCTCGCGCAAGTTTCGGTGGCGGAGCCCT 4446  
 3716 CCGTCCGCTCGGCGCATGCGGCTTTGAGCTCGCGCAAGTTTCGGTGGCGGAGCCCT 3657  
 4447 GATGCTCTTCGTCAGATCATCTGATCGAAGACCGGCTTCCATCCGAGTACGTGCTC 4506  
 3656 GATGCTCTTCGTCAGATCATCTGATCGAAGACCGGCTTCCATCCGAGTACGTGCTC 3597  
 4507 GCTCGATGCGATGTTTCGCTTGGTTCGAATGGGCGAGTAGCCGATCAAGCGTATGCA 4566  
 3596 GCTCGATGCGATGTTTCGCTTGGTTCGAATGGGCGAGTAGCCGATCAAGCGTATGCA 3537  
 4567 GCGCGCGCATTCGATCAGCCATGATGATATCTTCGCGGAGGAGCAAGTGAGATGACA 4626  
 3536 GCGCGCGCATTCGATCAGCCATGATGATATCTTCGCGGAGGAGCAAGTGAGATGACA 3477  
 4627 GAGATCTCTCCCGGCTTCCGCAATAGCAGCCGCTTCCGCTTTCAGTGACAA 4686  
 3476 GAGATCTCTCCCGGCTTCCGCAATAGCAGCCGCTTCCGCTTTCAGTGACAA 3417  
 4687 CGTCGAGCAGCTGCGCAAGAAACCGCTCGTGGCGAGCCACGATAGCCGCTGCTC 4746  
 3416 CGTCGAGCAGCTGCGCAAGAAACCGCTCGTGGCGAGCCACGATAGCCGCTGCTC 3357  
 4747 CGTCTCTGCAATTCATTCAGGGCACCGGACAGTTCGTCGATCAAAAAGAACCGGGGCG 4806  
 3356 CGTCTCTGCAATTCATTCAGGGCACCGGACAGTTCGTCGATCAAAAAGAACCGGGGCG 3297  
 4807 CCGTGGCTGACAGCGGAAACACCGCGCATCAGCAGCGGATTCGTTGTCGCCAGT 4866  
 3296 CCGTGGCTGACAGCGGAAACACCGCGCATCAGCAGCGGATTCGTTGTCGCCAGT 3237  
 4867 CATAGCGAATAGCTCTCCACCCAGCGGCGGAGAACCTGCGTGAATCCCATCTGTT 4926  
 3236 CATAGCGAATAGCTCTCCACCCAGCGGCGGAGAACCTGCGTGAATCCCATCTGTT 3177  
 4927 CAATCATCGAAACGATTCCTCATCTCTTCGATCAGATCTTCCTCGGCTC 4986  
 3176 CAATCATCGAAACGATTCCTCATCTCTTCGATCAGATCTTCCTCGGCTC 3117  
 4987 AGATCTTGGCGGCAAGAAAGCCATCAGTTTACTTTGCGGCTTCCCAACCTTACAG 5046  
 3116 AGATCTTGGCGGCAAGAAAGCCATCAGTTTACTTTGCGGCTTCCCAACCTTACAG 3057  
 5047 AGGCGCCCGCAGCTGGCAATTCGCTTTCGCTTTCGCTTCCCAATAAACCGCCAGCTAGCT 5106  
 3056 AGGCGCCCGCAGCTGGCAATTCGCTTTCGCTTTCGCTTCCCAATAAACCGCCAGCTAGCT 2997  
 5107 ATCCGCAATGTAAGCCCACTGCAAGTACCTCTTCTCTTTCGCGCTTCGCTTTCCCTTG 5166  
 2996 ATCCGCAATGTAAGCCCACTGCAAGTACCTCTTCTCTTTCGCGCTTCGCTTTCCCTTG 2937  
 5167 TCCAGATAGCCCGAGTACGATTCATCCCGGGGTACAGACCGTTTCTTCGCGACTGGCTT 5226  
 2936 TCCAGATAGCCCGAGTACGATTCATCCCGGGGTACAGACCGTTTCTTCGCGACTGGCTT 2877

QY 5227 TCTACGTTCCGCTTCCTTTAGAGCCCTTGGCGCCCTGAGTGTCTGGGAGCGTG 5283  
 Db 2876 TCTACGTTCCGCTTCCTTTAGAGCCCTTGGCGCCCTGAGTGTCTGGGAGCGTG 2820

RESULT 5  
 ID AAV33629/c  
 XX AAV33629 standard; DNA; 5594 BP.  
 AC AAV33629;  
 XX  
 DT 29-DEC-1998 (first entry)  
 XX  
 DE GENSA 981, a monomeric DNA sequence produced by the invention.  
 XX  
 KW Class IIS restriction endonuclease recognition site;  
 KW endogenous mouse promoter element; tissue-specific gene expression;  
 KW hormone-specific gene expression; ss;  
 KW developmental-specific gene expression.  
 XX  
 OS Synthetic.  
 XX  
 PN WO9838326-A1.  
 XX  
 PD 03-SEP-1998.  
 XX  
 PF 28-FEB-1998; 98WO-US003918.  
 XX  
 PR 28-FEB-1997; 97US-0070910P.  
 XX  
 PA (NATU-) NATURE TECHNOLOGY CORP.  
 XX  
 PI Hodgson CP, Zink MA, Xu G;  
 XX  
 DR WPI; 1998-495399/42.  
 XX  
 PT Method for assembling gene or gene vector - comprises use of primers  
 PT containing class IIS restriction endonuclease recognition sites.  
 XX  
 PS Example 2; Page 107-110; 141pp; English.  
 XX

The invention provides a novel method for directing self-assembly of a  
 gene having three or more fragments in a directionally and spatially  
 ordered fashion to produce a gene or a gene vector. The method involves  
 usage of primers, containing class IIS restriction endonuclease  
 recognition sites, for isolation of these fragments. As described in the  
 disclosure, the method may also use a vector for the incorporation and  
 screening of endogenous mouse promoter elements for the identification of  
 cell specific promoters. In the example given, plasmids pBK-CMV  
 (AAV33626), pVLMB (AAV33623) and pLONVGH-900 (AAV33621) were used as  
 templates from which six fragments were amplified. Each of the fragments  
 contained different regulatory sequences. The six PCR fragments were  
 designed to self-assemble into a retro-vector using the method of the  
 invention. The present sequence, designated as GENSA 981, represents the  
 monomeric DNA sequence of the six ligated fragments. In general, the  
 method is claimed to be useful for isolating and identifying regulatory  
 sequences from a cell, including those for enhanced biological activity,  
 or tissue-specific, hormone-specific or developmental-specific gene  
 expression

Sequence 5594 BP; 1232 A; 1519 C; 1518 G; 1325 T; 0 U; 0 Other;  
 Query Match 31.3%; Score 1652.4; DB 2; Length 5594;  
 Best Local Similarity 85.4%; Pred. No. 7.3e-242;  
 Matches 1916; Conservative 0; Mismatches 261; Indels 67; Gaps 4;

QY 3107 CGCGTGTGCGGCTTTTCCATAGGCTCCGCCCTTACAGGATCAAAAATCGAC 3166  
 Db 5591 CGCGGTTGTGCGGCTTTTCCATAGGCTCCGCCCTTACAGGATCAAAAATCGAC 5532

QY 3167 GCTCAAGTCAGAGTGGCGAAACCGACAGGACTATTAAGTACAGGCTTCCCGCTG 3226  
 Db

Db 5531 GCTCAAGTCAGAGTGGCGAAACCGACAGGACTATTAAGATACAGGGCTTTCCTCGT 5472  
 QY 3227 GAAGTCCCTCGTGGCTCTCTGTTCGACCTGCGCTTACCGGATACCTGTCCGCT 3286  
 Db 5471 GAAGTCCCTCGTGGCTCTCTGTTCGACCTGCGCTTACCGGATACCTGTCCGCT 5412  
 QY 3287 TTCTCCCTTCGGGAAGCGTGGCTTTCTCATAGCTACGCTGTAGTATCTCACTTCGG 3346  
 Db 5411 TTCTCCCTTCGGGAAGCGTGGCTTTCTCAATGCTACGCTGTAGGTATCTCACTTCGG 5352  
 QY 3347 TGTAGTGTCTGCTCCAAAGCTGGGCTGTGTGTCAGAAACCCCGCTTACGCGGACCGCT 3406  
 Db 5351 TGTAGTGTCTGCTCCAAAGCTGGGCTGTGTGTCAGAAACCCCGCTTACGCGGACCGCT 5292  
 QY 3407 GCGCTTTATCCGTTAACTATCTGCTTCTGAGTCCAAACCGGTTAAGACAGCTTATCGCAC 3466  
 Db 5291 GCGCTTTATCCGTTAACTATCTGCTTCTGAGTCCAAACCGGTTAAGACAGCTTATCGCAC 5232  
 QY 3467 TGGCAGCAGCCACTGTGTAACAGGATTAGCAGAGGAGTATGTAGGCGGTCTACAGAGT 3526  
 Db 5231 TGGCAGCAGCCACTGTGTAACAGGATTAGCAGAGGAGTATGTAGGCGGTCTACAGAGT 5172  
 QY 3527 TCTTGAAGTGGTGGCTTAACTAGCGCTACACTAGAAGAACAGTATTTGGTATCTCGGCTC 3586  
 Db 5171 TCTTGAAGTGGTGGCTTAACTAGCGCTACACTAGAAGAACAGTATTTGGTATCTCGGCTC 5112  
 QY 3587 TGCTGAAGCCAGTTACCTTCGGAAGAGTGTGGTAGCTCTTGATCCGCAAAACAAACCA 3646  
 Db 5111 TGCTGAAGCCAGTTACCTTCGGAAGAGTGTGGTAGCTCTTGATCCGCAAAACAAACCA 5052  
 QY 3647 CCGCTGTAGCGGTGGTGTGTTTGTGCAAGCAGCAGATTACGCGCAGAAACAAAGGAT 3706  
 Db 5051 CCGCTGTAGCGGTGGTGTGTTTGTGCAAGCAGCAGATTACGCGCAGAAACAAAGGAT 4992  
 QY 3707 CTCAGAAGATCTTTGATCTTTCTACGGGTCTGACGCTC-----AGTGGAGC 3757  
 Db 4991 GGTTGTGGGCTCTTTATTGAGCTCGGGAGCAGAAAGCGCGCAACAGAGCGAGAGCG 4932  
 QY 3758 AAAACTCAGTTAAGGATTTTGGTCAATGATTTATGTCGACAAAGCGGCAATCGTGC 3817  
 Db 4931 AACTGATGGTTAGTTCAAATAAGGCACAGGGTCAITTCAGGTCTTTGGGGCACCTTGA 4872  
 QY 3818 CTC-----CCCACTCTCTGAGTTCGGGGCATGAGTGCAGATAGCCGCTG 3864  
 Db 4871 AACATCTGATGGTTCTCTAGAATCTCTGAGGCTGACCGCATCTGGGACCATCTGTT 4812  
 QY 3865 CTGGTTTCTGATGCGGACGATTTTC-----ACTGCGGTAGAACTCCGCGAG 3914  
 Db 4811 CTGGCCCTGAGCGGGGCGAGAACTGCTTACCACAGATATCTGTTTGGCCCATATTCA 4752  
 QY 3915 GTGCTCCAGCTCAGCAGCAGCTGNAACCACTCGCGAGGGGATCGAGCCGGGTGGGG 3974  
 Db 4751 GCTGTTCCATCTGTTCTTGGCCCTGAGCGGGGCGAGAACTGCTTACCACAGATATCTG 4692  
 QY 3975 GAAGAACTCCAGCATGAGATCCCGCGCTGGAGGATCATCCAGCGGCGCTCCCGGAAAC 4034  
 Db 4691 TTTGGCCCATATTCAGCTGTTCCATCTGTTCTCTGACCTTGATCTGAACTTCTTATCTC 4632  
 QY 4035 GATTCCGAAGCCCAACCTTTTCATAGAAGCGCGGTGGAATCGAAATCTCG----- 4085  
 Db 4631 AGTTATGATTTTTCATGCTTGCATAAATGCGGTTACTTAAAGTAGCTTGCACAACTA 4572  
 QY 4086 -----TGATGGCAGGTTGGGCGTCTGCTTGGTTCGTTCAAT 4119  
 Db 4571 CAGTGGGGTCTTTCATTTCCCGCTTTTCTGGAGGTTGGGCGTCTGTTGGTTCGTT 4512  
 QY 4120 TCGAACCCAGAGTCCCGCTCAGAAAGAACTCGTCAAGAGGCGATAGAGGGGATCGCT 4179  
 Db 4511 TCGAACCCAGAGTCCCGCTCAGAAAGAACTCGTCAAGAGGCGATAGAGGGGATCGCT 4452  
 QY 4180 GCGAATCGGAGCGCGATACCGTAAAGCAGAGGAGCGGTGAGGATCGCCCAATTCGCGCCAA 4239  
 Db 4451 GCGAATCGGAGCGCGATACCGTAAAGCAGAGGAGCGGTGAGGATCGCCCAATTCGCGCCAA 4392







QY 3602 CCTTCGGAAGAAGTTGGTAGCTCTTGATCCGGGAACAAACCAACCGCTGGTAGCGGTG 3661  
 Db 4625 CCTTCGGAAGAAGTTGGTAGCTCTTGATCCGGGAACAAACCAACCGCTGGTAGCGGTG 4566  
 QY 3662 GTTTTGTGTTGTTGAAGCAGCAGATTTAGCGCAGAAAGGATCTCAGAAATCCTT 3721  
 Db 4565 GTTTTGTGTTGTTGAAGCAGCAGATTTAGCGCAGAAAGGATCTCAGAAATCCTT 4506  
 QY 3722 TGATCTTTTCTACGGGCTCTGACGCTCAGTGAACGAAACCTCAGCTTAAGGGATTTTGG 3781  
 Db 4505 TGATCTTTTCTACGGGCTCTGACGCTCAGTGAACGAAACCTCAGCTTAAGGGATTTTGG 4446  
 QY 3782 TCATGAGATTAATC----- 3794  
 Db 4445 TCATGAGATTAATCAAAAAGGATCTTCACTAGATCCTTTTAAATTAATAATGAAGTTTAA 4386  
 QY 3795 -----GTCGACCA 3802  
 Db 4385 GCACGTGTCAGTCTGCTCTCGGCCACGAGTGCAAGTGCAAGTGTCGGCGCGGGTCGGCA 4326  
 QY 3803 AAGCGGCATCGTCCCTCCCACTCTCTGAGTTTCGGGGGCATGATCGCGGATAGCCGC 3862  
 Db 4325 GGGCGAACTCCCGCCCAACCGGTGCTCGCGATCTCGGTATGCGCGGCCGAGCGGT 4266  
 QY 3863 TGTCTGTTTCTGATGCCAGGATTTGACTCCCGGTAGAACTCCGCGAGGTCTGCTCA 3922  
 Db 4265 CCGGAAAGTTCTGTGACACAGCACTCCGACCTCGCGGTACAGCTCTCGAGCGCGGCA 4206  
 QY 3923 GCC----- 3925  
 Db 4205 CCCACACCCAGGCCAGGTTGTTGTCGGCACCACTGCTGCTGGAACCGCGCTGATGAACA 4146  
 QY 3926 ----TCAGGCGAGCTGAACAACTCGCAGGGGATCGAGCCCGGGTGGCGAAGAACT 3982  
 Db 4145 GGGTCACGTCGTCCTCCGAGCACACCGCGAAGTCGTCCTCCACGAATCCCGGGAGAAC 4086  
 QY 3983 CCAGCATGAGATCCCGCGCTGGAGGATCATCCAGCGCGGTCCGGAAACGAATCCGA 4042  
 Db 4085 CGAGCGGTGCGTTCAGAACTCAGACCGCTCCGGCAGCTCGCGCGGTGAGCACCGGA 4026  
 QY 4043 AGCCCAACCTTTTCATAGAAGCGCGGTGGAATCGAAATCTCGTGATGGCAGGTTGGCG 4102  
 Db 4025 CGSCATGTTCACTTGGCCATGTTGGCCCTCTCAGTCTATTAATTGAAGCATTTATC 3966  
 QY 4103 TGCCTTGGTGGTCAATTTGAAACCCAGAGTCCCG----- 4137  
 Db 3965 AGGGTTATTGCTCTCATGAGCGGATACATATTTGAATGTAATTAGAAAAATAACAAATAG 3906  
 QY 4138 ----- 4137  
 Db 3905 GGGTTCGGCGCATTTTCCCGAAAAAGTGCCACCTGTATGCGGTGTGAATAACCGCACAG 3846  
 QY 4138 -----CTCAGAAGAACTC 4150  
 Db 3845 ATGCGTAAGAGAAAAATACGCATCAGAAATTTGAAGCGTTAATAATTTCAGAAAGACTC 3786  
 QY 4151 GTCAGAAGCGGATAGAGCGGATGCGTTCGGAATCGGAGCGCGGATACCGTAAAGCAC 4210  
 Db 3785 GTCAGAAGCGGATAGAGCGGATGCGTTCGGAATCGGAGCGCGGATACCGTAAAGCAC 3726  
 QY 4211 GAGGAAGCGGTGAGCCCATTCGCGCCCAAGCTCTTCAGCAATATCAGGATGCCAACGC 4270  
 Db 3725 GAGGAAGCGGTGAGCCCATTCGCGCCCAAGCTCTTCAGCAATATCAGGATGCCAACGC 3666  
 QY 4271 TATGTCCTGATAGCGGTGCGGCACACCCAGCGCGGCACAGTCGATCAATCCGAAAGCG 4330  
 Db 3665 TATGTCCTGATAGCGGTGCGGCACACCCAGCGCGGCACAGTCGATCAATCCGAAAGCG 3606  
 QY 4331 GCATTTTCCACATGATATTGGCAAGCAGGCGATCGCCATGGGTTCACGACGAGATCTCTC 4390  
 Db 3605 GCCATTTTCCACATGATATTGGCAAGCAGGCGATCGCCATGGGTTCACGACGATCTCTC 3546  
 QY 4391 GCCGTGGGCATCGCGGCTTTGAGCCTTGGCGAACAGTTGCGGTGGCGCGAGCCCTTGATG 4450

Db 3545 GCCGTGGGCATGCTCGCCTTGAGCCTGGCGAAACAGTTGCGCTGGCGGAGCCCTGATG 3486  
 QY 4451 CTCTTCCTCAGATCATCTCTGATCGAACAGCCGGCTTCCATCCGAGTACGTGCTCGCTC 4510  
 Db 3485 CTCTTCCTCAGATCATCTCTGATCGAACAGCCGGCTTCCATCCGAGTACGTGCTCGCTC 3426  
 QY 4511 GATCGGATGTTTCCGCTTGGTTCGATGGCAGGTAGCCGGATCAAGCGTATGACGCG 4570  
 Db 3425 GATCGGATGTTTCCGCTTGGTTCGATGGCAGGTAGCCGGATCAAGCGTATGACGCG 3366  
 QY 4571 CCGCATTTGCATAGCCATGATGATATCTTCTCGGCAGGACAAAGGTGAGATGACAGGAG 4630  
 Db 3365 CCGCATTTGCATAGCCATGATGATATCTTCTCGGCAGGACAAAGGTGAGATGACAGGAG 3306  
 QY 4631 ATCTGCCCCGGACATTTGCGCCCAATAGCAGCAGTCCCTTCCCGCTTCAAGTGAACAGCTC 4690  
 Db 3305 ATCTGCCCCGGACATTTGCGCCCAATAGCAGCAGTCCCTTCCCGCTTCAAGTGAACAGCTC 3246  
 QY 4691 GAGCACAGCTGCGCAAGGAAACCGCGTCGTCGCGCAGCAGTACGATAGCGCTGCTCGTC 4750  
 Db 3245 GAGCACAGCTGCGCAAGGAAACCGCGTCGTCGCGCAGCAGTACGATAGCGCTGCTCGTC 3186  
 QY 4751 CTGAGTTTCAATCAGGSCACCGGACAGTCTTTCACAAAAAGAACCGGCGCCCTCG 4810  
 Db 3185 TTGAGTTTCAATCAGGSCACCGGACAGTCTTTCACAAAAAGAACCGGCGCCCTCG 3126  
 QY 4811 CGTGCAGCGGAAACAGCGCGGATCAGAGCAGCCGATTCGTGTTGTGCCAGTCAAT 4870  
 Db 3125 CGTGCAGCGGAAACAGCGCGGATCAGAGCAGCCGATTCGTGTTGTGCCAGTCAAT 3066  
 QY 4871 GCCCAATAGCTCTCCACCCCAAGCGCGGAGAACCTCGCTGCAATCCATCTTGTTCAT 4930  
 Db 3065 GCCCAATAGCTCTCCACCCCAAGCGCGGAGAACCTCGCTGCAATCCATCTTGTTCAT 3006  
 QY 4931 CATGCGAAACGATCTCTCTCTCTTTCATCAGATCTTTCATCCCTGCGCCATCAGAT 4990  
 Db 3005 CATGCGAAACGATCTCTCTCTCTTTCATCAGATCTTTCATCCCTGCGCCATCAGAT 2946  
 QY 4991 CCTTGGCGGCAAGAACCATCCAGTTTTCAGAGGCTTCCCAACCTTACAGAGG 5050  
 Db 2945 CCTTGGCGGCAAGAACCATCCAGTTTTCAGAGGCTTCCCAACCTTACAGAGG 2886  
 QY 5051 CGCCCCAGCTGGCAATTCGGTTTCGCTGCTGTCATTAACCGCCAGTCTAGCTATCG 5110  
 Db 2885 CGCCCCAGCTGGCAATTCGGTTTCGCTGCTGTCATTAACCGCCAGTCTAGCTATCG 2826  
 QY 5111 CCATGTAAGCCCACTGCAAGTACCTGCTTCTCTTTGGCTTGGCTTTTCCCTTGTCCA 5170  
 Db 2825 CCATGTAAGCCCACTGCAAGTACCTGCTTCTCTTTGGCTTGGCTTTTCCCTTGTCCA 2766  
 QY 5171 GATAGCCCACTGAGCTGACATTCATCCGGGTGACGACCGTTTCTGCGGAGTGGCTTCTA 5230  
 Db 2765 GATAGCCCACTGAGCTGACATTCATCCGGGTGACGACCGTTTCTGCGGAGTGGCTTCTA 2706  
 QY 5231 CGTG 5234  
 Db 2705 CGTG 2702

RESULT 8  
 AAV33630/c  
 ID AAV33630 standard; DNA; 6561 BP.  
 XX AAV33630;  
 AC AAV33630;  
 XX  
 DT 29-DEC-1998 (first entry)  
 XX  
 DE Plasmid VLSNO2 DNA sequence used in the method of the invention.  
 XX  
 KW Class IIS restriction endonuclease recognition site; IIR;  
 endogenous mouse promoter element; tissue-specific gene expression;  
 hormone-specific gene expression; mouse VL30 genome;  
 KW



KW developmental-specific gene expression; long terminal repeat; ss.  
XX Synthetic.  
OS WO9838326-A1.  
XX  
XX  
XX  
XX 03-SEP-1998.  
XX  
XX 28-FEB-1998; 98WO-US003918.  
XX  
XX 28-FEB-1997; 97US-0070910P.  
XX  
XX (NATU-) NATURE TECHNOLOGY CORP.  
XX  
XX Hodgson CP, Zink MA, Xu G;  
XX WPI; 1998-495399/42.  
XX  
XX Method for assembling gene or gene vector - comprises use of primers  
XX containing class IIS restriction endonuclease recognition sites.  
XX  
XX Example 3; Page 110-113; 141pp; English.  
XX  
XX The invention provides a novel method for directing self-assembly of a  
XX gene having three or more fragments in a directionally and spatially  
XX ordered fashion to produce a gene or a gene vector. The method involves  
XX usage of primers, containing class IIS restriction endonuclease  
XX recognition sites, for isolation of these fragments. As described in the  
XX disclosure, the method may also use a vector for the incorporation and  
XX screening of endogenous mouse promoter elements for the identification of  
XX cell specific promoters. In the example given, plasmid VLSNO2, containing  
XX a circularly permuted mouse VLSO genome, was used in the construction of  
XX single long terminal repeat (LTR) vectors used in the method of the  
XX invention. In general, the method is claimed useful for isolating and  
XX identifying regulatory sequences from a cell, including those for  
XX enhanced biological activity, or tissue-specific, hormone-specific or  
XX developmental-specific gene expression  
XX  
XX Sequence 6561 BP; 1629 A; 1593 C; 1696 G; 1643 T; 0 U; 0 Other;  
XX  
XX Query Match 30.6%; Score 1618.2; DB 2; Length 6561;  
XX Best Local Similarity 86.7%; Pred. No. 1.1e-236;  
XX Matches 1911; Conservative 0; Mismatches 23; Indels 269; Gaps 1;  
XX  
XX 3081 GCAAAAGGCCAGGAAACCGTAAAGCCCGGTGCTGGCGTTTTCATAGGCTCGGCC 3140  
XX  
XX 2305 GCAGGTGTACTCGAGCGCGCATCTCGGCGTTGCTGGCGTTTTCATAGGCTCGGCC 2246  
XX  
XX 3141 CCTGTACGAGCATCACAATAATCGAGCTCAAGTCAGAGTGGCGAAACCCGACAGACT 3200  
XX  
XX 2245 CCTGTACGAGCATCACAATAATCGAGCTCAAGTCAGAGTGGCGAAACCCGACAGACT 2186  
XX  
XX 3201 ATAAAGATACCGGCGTTTCCCGCTGGAAGCTCCCTGTCGCTCTCTGTTTCCGACCT 3260  
XX  
XX 2185 ATAAAGATACCGGCGTTTCCCGCTGGAAGCTCCCTGTCGCTCTCTGTTTCCGACCT 2126  
XX  
XX 3261 GCGCTTACCGGATACCTGTCCGCTTCTCCCTTCGGGAAGCGTGGCGTTTCTCATAG 3320  
XX  
XX 2125 GCGGCTTACCGGATACCTGTCCGCTTCTCCCTTCGGGAAGCGTGGCGTTTCTCAATG 2066  
XX  
XX 3321 CTCACGCTGTAGTATCTCAGTTCCGTTGAGTGTCTGCTCCCAAGCTGGGCTGTGTGA 3380  
XX  
XX 2065 CTCACGCTGTAGTATCTCAGTTCCGTTGAGTGTCTGCTCCCAAGCTGGGCTGTGTGA 2006  
XX  
XX 3381 CGAAACCCCGCTTACGCGGACCGCTCGCGCTTATCCGTTAATCTGTTTCCGTTCCAA 3440  
XX  
XX 2005 CGAAACCCCGCTTACGCGGACCGCTCGCGCTTATCCGTTAATCTGTTTCCGTTCCAA 1946  
XX  
XX 3441 CCGGTTAAGACAGACTTATCGCACTGGCAGCAGCCACTGGTAACAGGATTAAGCAGAGC 3500  
XX  
XX 1945 CCGGTTAAGACAGACTTATCGCACTGGCAGCAGCCACTGGTAACAGGATTAAGCAGAGC 1886  
XX  
XX 3501 GAGGTATGTAGCGGTCTACAGAGTTCTTTGAAGTGGTGGCCCTAACTACGGCTACACTAG 3560

Db 1885 GAGGTATGTAGCGGTCTACAGAGTTCTTGAAGTGGTGGCTAACTACGGCTACACTAG 1826  
QY 3561 AAGAACAGTATTTGGTATCTCGGCTCTCTGAAGCCAGTTTACCTTCGGAAGAGAGTTGG 3620  
Db 1825 AAGGACAGTATTTGGTATCTCGGCTCTCTGAAGCCAGTTTACCTTCGGAAGAGAGTTGG 1766  
QY 3621 TAGCTCTTGATCCGCGCAACAAACACCGCTGGTAGCGTGGTGGTGGTGGTGGTGGTGGTGG 3680  
Db 1765 TAGCTCTTGATCCGCGCAACAAACACCGCTGGTAGCGTGGTGGTGGTGGTGGTGGTGGTGG 1706  
QY 3681 GCAGATTACCGCGCAGAAAAAAGGATCTCAAGAGATCCTTTGATCTTTTCTACGGGTC 3740  
Db 1705 GCAGATTAG----- 1696  
QY 3741 TGACGCTCAGTGAACGAAACTCAGTTAAGGGATTTTGGTCATGAGATTATCTGTCGAC 3800  
Db 1695 ----- 1696  
QY 3801 CAAAGCGGCATCGTGCCTCCACTCTCTGCAAGTTTCGGGGGCATGATCGCGGATAGCC 3860  
Db 1695 ----- 1696  
QY 3861 GCTGCTGTTTCTCGATGCCGATGCGAGATTGCACTCCGCGGTAGAACTCCGCGAGGTCGTC 3920  
Db 1695 ----- 1696  
QY 3921 CAGCCTCAGGACAGCTGAAACCACTCCGAGGGGATCGAGCCGGGTGGCGGAAGAA 3980  
Db 1695 -----AATTCGGGTGGCGGAAGAA 1675  
QY 3981 CTCAGCATGATCCCCCGCTGAGGATCATCCAGCGGGTCCCGAAAAACGATTCC 4040  
Db 1674 CTCAGCATGATCCCCCGCTGAGGATCATCCAGCGGGTCCCGAAAAACGATTCC 1615  
QY 4041 GAAGCCCAACCTTTCATAGAGCGGCGGTGGAATCGAAATCTCGTATGCGAGGTTGG 4100  
Db 1614 GAAGCCCAACCTTTCATAGAGCGGCGGTGGAATCGAAATCTCGTATGCGAGGTTGG 1555  
QY 4101 CGTCGCTTGGTGGTCACTTTCGAAACCCAGAGTCCCGCTCAGAAGAACTCGTCAAGAAAG 4160  
Db 1554 CGTCGCTTGGTGGTCACTTTCGAAACCCAGAGTCCCGCTCAGAAGAACTCGTCAAGAAAG 1495  
QY 4161 CGATAGAGCGGATCGCTGCGAATCGGAGCGGCGATACCGTAAACACGAGAAAGCGG 4220  
Db 1494 CGATAGAGCGGATCGCTGCGAATCGGAGCGGCGATACCGTAAACACGAGAAAGCGG 1435  
QY 4221 TCAGCCCATTCGCGCCAAAGCTTTCAGCAATATCAAGGATAGCCAAACGATATGCTCTGA 4280  
Db 1434 TCAGCCCATTCGCGCCAAAGCTTTCAGCAATATCAAGGATAGCCAAACGATATGCTCTGA 1375  
QY 4281 TAGCGTCCGCGCACACCCAGCGGCCACAGTCGATGAATCCAGAAAGCGGCCATTTTC 4340  
Db 1374 TAGCGTCCGCGCACACCCAGCGGCCACAGTCGATGAATCCAGAAAGCGGCCATTTTC 1315  
QY 4341 ACCATGATATTCGCGCAAGCAGGATCGCCATGCGGTACACGAGATCTCCCGCTCGGC 4400  
Db 1314 ACCATGATATTCGCGCAAGCAGGATCGCCATGCGGTACACGAGATCTCCCGCTCGGC 1255  
QY 4401 ATCGCGCTTGAAGCTTGGGAAACAGTTTGGTGGCGGAGCCCTGATGCTCTTCGTC 4460  
Db 1254 ATCGCGCTTGAAGCTTGGGAAACAGTTTGGTGGCGGAGCCCTGATGCTCTTCGTC 1195  
QY 4461 AGATCATCTGTATCGAAGACCGGCTTCCATCCGAGTACGTCGCTCGATGCGATGT 4520  
Db 1194 AGATCATCTGTATCGAAGACCGGCTTCCATCCGAGTACGTCGCTCGATGCGATGT 1135  
QY 4521 TTGCTTGGTGGTGAATGGCGAGGTAGCGGATTAAGCGTATGCGAGCGCGCGATGCA 4580  
Db 1134 TTGCTTGGTGGTGAATGGCGAGGTAGCGGATTAAGCGTATGCGAGCGCGCGATGCA 1075  
QY 4581 TCAGCATGATGATCTTTCGCGAGGAGCAAGGTGAGATGACAGAGATCTCTGCCCC 4640



550	AAACCCGACAGACATATAAAGATACAGCGCTTTCCCTCGAAGCTCCCTCGTCGGCTC	609
3246	TCCTGTTCCGACCCCTCCGCTTACCGGATACCTGTCCGCTTTCTCCCTTCGGGAAGCGT	3305
610	TCCTGTTCCGACCCCTCCGCTTACCGGATACCTGTCCGCTTTCTCCCTTCGGGAAGCGT	669
3306	GGCGCTTTCATAGCTACGCTGTAGGTATCTCAGTTCCGGTGTAGGTCTGTCGCTCCAA	3365
670	GGCGCTTTCATAGCTACGCTGTAGGTATCTCAGTTCCGGTGTAGGTCTGTCGCTCCAA	729
3366	GCTGGCTGTGTGCAGAAACCCCGCTTCAGCCCGACCGCTCGGCTTATCCGGTAACTA	3425
730	GCTGGCTGTGTGCAGAAACCCCGCTTCAGCCCGACCGCTCGGCTTATCCGGTAACTA	789
3426	TGCTCTTGAGTCAACCCCGGTAAAGACAGACTTATCGCACCTGGCAGACCACTGGTAA	3485
790	TCGCTCTTGAGTCAACCCCGGTAAAGACAGACTTATCGCACCTGGCAGACCACTGGTAA	849
3486	CAGGATTAGCAGAGCAGGTATCTAGCGGTGCTACAGAGTTCTTGAAGTGGTGGCCTAA	3544
850	CAGATTAGCAGAGCAGGTATCTAGCGGTGCTACAGAGTTCTTGAAGTGGTGGCCTAA	909
3546	CTACGGCTACACTAGAAAGAACAGTATTTGGTATCTCGCTCTGCTGAAGCAGTACCTT	3605
910	CTACGGCTACACTAGAAAGAACAGTATTTGGTATCTCGCTCTGCTGAAGCAGTACCTT	969
3606	CGGAAAAAGAGTTGGTAGCTCTTGATCCGCAACAAACACCGCTGGTAGCGGTGTTT	3665
970	CGGAAAAAGAGTTGGTAGCTCTTGATCCGCAACAAACACCGCTGGTAGCGGTGTTT	1029
3666	TTTTGTTTCAAGCAGCAGATTACGCGCAGAAAAAAGGATCTCAAGAAAGTACCTTTGAT	3725
1030	TTTTGTTTCAAGCAGCAGATTACGCGCAGAAAAAAGGATCTCAAGAAAGTACCTTTGAT	1089
3726	CTTTTCTACGGGGTCTCAGCGTCACTGGAACGAAACTCAGGTTAAGGATTTTGTCAT	3785
1090	CTTTTCTACGGGGTCTCA-----	1107
3786	GAGATTATCGTCGACCAAGCGGCCATCGTGCCTCCCACTCTCGATCGTGGGGCATG	3845
1108	-----	1107
3846	GATCGCGGATAGCCGCTGCTGTTTCTCGATGCGCAGCGANTTGCACTGCCGTTAGAA	3905
1108	-----	1107
3906	CTCCGCGAGGTCTCCAGCCTCAGGCAGCAGCTGAACCAACTCGCAGGGGATCGAGCCC	3965
1108	-----	1107
3966	GGGTTGGCGAAGAACTCCAGATGATCCCGCGCTGGAGGATCATCAGCCGCGCTC	4025
1108	-----	1107
4026	CCGGAAAAACGATTCGGAAGCCCACTTTTCATAGAGCGCGGTGGAAATCGAAATCTCG	4085
1108	-----	1107
4086	TGATGGCAGTTGGGCGTTCGCTTGGTCCGTCATTTCCGAAACCCAGAGTCCCGCTCAGAAG	4145
1108	-----CGTCCAGAAG	1117
4146	AACCTGTCAGAAAGCGGATAGAGCGGATGCGCTTGGAAATCGGAGCGGCGATACCGTAA	4205
1118	AACCTGTCAGAAAGCGGATAGAGCGGATGCGCTTGGAAATCGGAGCGGCGATACCGTAA	1177
4206	AGCAGGGAACCGGTACGCCCATTTCGCGCCAAAGCTCTTCAGCAATATCACGGGTAGCC	4265
1178	AGCAGGGAACCGGTACGCCCATTTCGCGCCAAAGCTCTTCAGCAATATCACGGGTAGCC	1237
4266	AACGCTATGTCTGATAGCGGTCCGCCACACCCAGCGCGGCCACAGTGTGATGATTCAGAA	4325
1238	AACGCTATGTCTGATAGCGGTCCGCCACACCCAGCGCGGCCACAGTGTGATGATTCAGAA	1297

QY	4326	AAGCGGCATTTTCCACCATGATATTTCGGCAAGCAGGCATTCGCCATCTGGTTCACGACGAGA	4388
Db	1298	AAGCGGCATTTTCCACCATGATATTTCGGCAGCAGGCATCGCCATGGGTACGACGAGA	1357
QY	4386	TCCTCGCCGTTCGGGCATCGCGCTTTAGAGCTTCGGCAAAGTTTCGGGTGGCGGAGGCC	4445
Db	1358	TCCTCGCCGTTCGGGCATCGCGCTTTAGAGCTTCGGCAAAGTTTCGGGTGGCGGAGGCC	1417
QY	4446	TGATGCTCTTTCGTCAGATCATCTTGATCGACAAGACCGGCTTCCATCCGAGTACGTGCT	4505
Db	1418	TGATGCTCTTTCGTCAGATCATCTTGATCGACAAGACCGGCTTCCATCCGAGTACGTGCT	1477
QY	4506	CGCTCGATCGATGTTTTCGCTTCGGTGGTGGAAATGGCAGGTAGCCGATCAAGCGGTATGC	4565
Db	1478	CGCTCGATCGATGTTTTCGCTTCGGTGGTGGAAATGGCAGGTAGCCGATCAAGCGGTATGC	1537
QY	4566	AGCGCGCGCATTCGATCAGCCATGATGATPACTTTTCTTCGGCAGGAGCAAGGTAGATGAC	4625
Db	1538	AGCGCGCGCATTCGATCAGCCATGATGATPACTTTTCTTCGGCAGGAGCAAGGTAGATGAC	1597
QY	4626	AGGAGATCTTCGCCCGGCACTTCGCCCAATAGCAGCCAGTCCCTTCCCGCTTCAGTGACA	4685
Db	1598	AGGAGATCTTCGCCCGGCACTTCGCCCAATAGCAGCCAGTCCCTTCCCGCTTCAGTGACA	1657
QY	4686	ACGTTCGAGCACAGCTTCGCGCAGGAAACGCCCGTTCGTGGCCAGCCAGATAGCGCGCTGCC	4745
Db	1658	ACGTTCGAGCACAGCTTCGCGCAGGAAACGCCCGTTCGTGGCCAGCCAGATAGCGCGCTGCC	1717
QY	4746	TCGTCCTCGAGTTTCATTTCAGGGCACCGGACAGGTCGGTCTTTGACAAAAGAACCGGGCGC	4805
Db	1718	TCGTCCTCGAGTTTCATTTCAGGGCACCGGACAGGTCGGTCTTTGACAAAAGAACCGGGCGC	1777
QY	4806	CCCTGCGCTGACAGCCGGAACACGGCGGCATCAGACAGCCGATTCGTTGTGCCAG	4865
Db	1778	CCCTGCGCTGACAGCCGGAACACGGCGGCATCAGACAGCCGATTCGTTGTGCCAG	1837
QY	4866	TCATAGCGGAATAGCCTCTCCACCAAGCGGCGGAGAACTCGGTGCAATCCATCTTGT	4925
Db	1838	TCATAGCGGAATAGCCTCTCCACCAAGCGGCGGAGAACTCGGTGCAATCCATCTTGT	1897
QY	4926	TCAATCATGGAATAGATTCCTTCATCTGTCCTTCGTGATCAGATCTTGATCCCTCGGCCAT	4985
Db	1898	TCAATCATGGAATAGATTCCTTCATCTGTCCTTCGTGATCAGATCTTGATCCCTCGGCCAT	1957
QY	4986	CAGATCTTCGCGCAAGAACCATCCAGTTTACTTTTGCAGGCTTCCCAACCTTACCA	5045
Db	1958	CAGATCTTCGCGCAAGAACCATCCAGTTTACTTTTGCAGGCTTCCCAACCTTACCA	2017
QY	5046	GAGGCGCCCCAGCTGGCAATTCGGGTTTCGCTTCGTGTCATATAAACCGCCAGCTTAGC	5105
Db	2018	GAGGCGCCCCAGCTGGCAATTCGGGTTTCGCTTCGTGTCATATAAACCGCCAGCTTAGC	2077
QY	5106	TATCGCCATGTAAGCCCACTGCAAGTACCTGCTTCTCTT	5146
Db	2078	AACCTGTTGGGAAGGGCGCATTCGGTGGCGGCGCTTCCTGCTATT	2118

RESULT 10  
ABQ78293  
ID ABQ78293 standard: DNA: 3534 BP:

XX ABQ78293;

XX  
DT 05-NOV-2002 (first entry)

XX DE Nucleotide sequence of vector pSPC5-12-HV-GHRH.

pig; growth hormone releasing hormone; GHRH; growth rate; lean body mass;  
 Insulin-like Growth Factor-I; IGF-I; milk production; feed efficiency;  
 somatotroph; growth-related disorder; hypopituitary dwarfism;  
 meat production; egg production; ss.

OS Synthetic.  
 PN WO200261037-A2.  
 XX 08-AUG-2002.  
 PD 12-DEC-2001; 2001WO-US048726.  
 XX 12-DEC-2000; 2000US-0255021P.  
 PR (BAYU ) BAYLOR COLLEGE MEDICINE.  
 XX (ADVI-) ADVISYS.  
 PA Schwartz RJ, Carpenter RH, Draghia-Akli R, Kern DR, Smith RG;  
 PI WPI; 2002-619237/66.  
 DR Improving or enhancing growth, lean body mass, milk production, feed  
 PT efficiency or Insulin-like Growth Factor-I levels, comprises introducing  
 PT a vector encoding a growth hormone releasing hormone into an animal  
 PT before or during gestation.  
 XX  
 PS Example 2; Page 109-111; 113pp; English.  
 XX  
 CC The present sequence represents vector pSPc5-12-HV-GHRH, which carries  
 CC cDNA encoding pig growth hormone releasing hormone (GHRH) cDNA. Nucleic  
 CC acids encoding GHRH are used in the method of the invention. The  
 CC specification describes a method for improving or enhancing  
 CC characteristics e.g. growth, lean body mass, Insulin-like Growth Factor  
 CC (IGF)-I levels, growth rate and milk production in an offspring, and for  
 CC delaying birth of an offspring. The method comprises introducing a  
 CC vector, encoding GHRH, into cells of the female animal prior to or during  
 CC gestation of the offspring under conditions where the nucleotide sequence  
 CC is expressed. The method is useful of improving or enhancing animal  
 CC growth, for increasing growth hormone, lean body mass, IGF-I levels, feed  
 CC efficiency, growth rate, ratio of somatotrophs to other hormone-producing  
 CC cells in a pituitary gland, and milk production in an offspring, and for  
 CC delaying birth of an offspring. GHRH nucleic acids and vectors are used  
 CC for diagnostic purposes in clinical medicine, both human and veterinary.  
 CC e.g. in treating growth-related disorders such as hypopituitary dwarfism  
 CC resulting from abnormalities in growth hormone production, and in  
 CC stimulating the growth and enhancing feed conversion efficiency of  
 CC animals raised for meat, milk and egg production  
 XX  
 SQ Sequence 3534 BP; 764 A; 1018 C; 979 G; 773 T; 0 U; 0 Other;  
 Query Match 30.4%; Score 1603.8; DB 6; Length 3534;  
 Best Local Similarity 82.8%; Pred. No. 1.8e-234;  
 Matches 2022; Conservative 0; Mismatches 27; Indels 392; Gaps 1;  
 QY 2706 CTAGACGTAATCATGTCATAGCTGTTTCTGTGTGAATTTGTTATCCGCTCACAAATCC 2765  
 DB 1412 CTTGGCGTAATCATGTCATAGCTGTTTCTGTGTGAATTTGTTATCCGCTCACAAATCC 1471  
 QY 2766 ACACAAACATACGACGCGGAAGCATAAAGTAAAGCTGGGTGCTTAATGAGTGAGCTA 2825  
 DB 1472 ACACAAACATACGACGCGGAAGCATAAAGTAAAGCTGGGTGCTTAATGAGTGAGCTA 1531  
 QY 2826 ACTCAATTAATTTGGTTCGCTCACTGCGCGGTTCACAGTCCGGAACCTCTCGTGCCA 2885  
 DB 1532 ACTCAATTAATTTGGTTCGCTCACTGCGCGGTTCACAGTCCGGAACCTCTCGTGCCA 1591  
 QY 2886 GCTGCATTAATGAATCGGCCAACGCGCGGGAGAGCGGTTTTCGTTATTTGGCGCTCTTC 2945  
 DB 1592 GCTGCATTAATGAATCGGCCAACGCGCGGGAGAGCGGTTTTCGTTATTTGGCGCTCTTC 1651  
 QY 2946 CGCTTCCTCGCTCACTGACTCGCTCGCTCGCTCGCTCGCTCGCTCGCTCGCTCGCTCGC 3005  
 DB 1652 CGCTTCCTCGCTCACTGACTCGCTCGCTCGCTCGCTCGCTCGCTCGCTCGCTCGCTCGC 1711  
 QY 3006 TCACCTCAAGGCGGTAATACGGTTATCCACAGAATCAGGGGATACGCGAGGAAGACAT 3065  
 DB 1712 TCACCTCAAGGCGGTAATACGGTTATCCACAGAATCAGGGGATACGCGAGGAAGACAT 1771

QY 3066 GTGACCAAGGCGCAGCAAAAGGCCAGAACCGTAAAAAGGCCGCGTGTGCTGGCGTTTTT 3125  
 DB 1772 GTGACCAAGGCGCAGCAAAAGGCCAGAACCGTAAAAAGGCCGCGTGTGCTGGCGTTTTT 1831  
 QY 3126 CCATAGGCTCGCGCCCTCTGACGAGCATCAAAAATCGACGCTCAAGTCAAGTGAGGCGG 3185  
 DB 1832 CCATAGGCTCGCGCCCTCTGACGAGCATCAAAAATCGACGCTCAAGTCAAGTGAGGCGG 1891  
 QY 3186 AAACCCGACAGGACTATAAAGATACAGGCGGTTTTCCCTCGAAAGCTCCCTCGTGGCTC 3245  
 DB 1892 AAACCCGACAGGACTATAAAGATACAGGCGGTTTTCCCTCGAAAGCTCCCTCGTGGCTC 1951  
 QY 3246 TCCGTTCGACCCCTCGCGCTTACGGATACCTGTCGCGCTTTCTCCCTCGGAAGCGT 3305  
 DB 1952 TCCGTTCGACCCCTCGCGCTTACGGATACCTGTCGCGCTTTCTCCCTCGGAAGCGT 2011  
 QY 3306 GCGGCTTTCTCATAGCTCAGCTGATAGTATCTCAGTTCCGCTGAGTTCGTTCCGCTCAA 3365  
 DB 2012 GCGGCTTTCTCATAGCTCAGCTGATAGTATCTCAGTTCCGCTGAGTTCGTTCCGCTCAA 2071  
 QY 3366 GCTGGGCTGTGCAAGAACCCCGCTTACGCGCGACCGCTGCGCTTATCCGTAACCTA 3425  
 DB 2072 GCTGGGCTGTGCAAGAACCCCGCTTACGCGCGACCGCTGCGCTTATCCGTAACCTA 2131  
 QY 3426 TCGTCTTTGAGTCCAAACCCGCTAAGACACGACTTATGCGCACTGGCAGCAGCCTGTGTA 3485  
 DB 2132 TCGTCTTTGAGTCCAAACCCGCTAAGACACGACTTATGCGCACTGGCAGCAGCCTGTGTA 2191  
 QY 3486 CAGGATTAGCAGAGCAGGATGATGAGCGGTGCTACAGAGTCTTGAAGTGGTGGCCTAA 3545  
 DB 2192 CAGGATTAGCAGAGCAGGATGATGAGCGGTGCTACAGAGTCTTGAAGTGGTGGCCTAA 2251  
 QY 3546 CTAGCGTCACTAGAGAACAGTATTTGATATCTGCGCTCTGCTGAAGCAGGTAACCTT 3605  
 DB 2252 CTAGCGTCACTAGAGAACAGTATTTGATATCTGCGCTCTGCTGAAGCAGGTAACCTT 2311  
 QY 3606 CGGAAAAAGAGTTGAGTCTTTGATCCGCGCAAAACCAACCGCTGGTGAAGCGGTGTTTT 3665  
 DB 2312 CGGAAAAAGAGTTGAGTCTTTGATCCGCGCAAAACCAACCGCTGGTGAAGCGGTGTTTT 2371  
 QY 3666 TTTTGTTCGCAAGCAGCAGATTACGCGCAGAAAAAGAGATCTCAAGAGAGATCCTTTGAT 3725  
 DB 2372 TTTTGTTCGCAAGCAGCAGATTACGCGCAGAAAAAGAGATCTCAAGAGAGATCCTTTGAT 2431  
 QY 3726 CTTTCTACGGGTCTGACGCTCAGTGGAAACGAAACTCACGTTAAGGGATTTTGGTCA 3785  
 DB 2432 CTTTCTACGGGTCTGACGCTCAGTGGAAACGAAACTCACGTTAAGGGATTTTGGTCA 2449  
 QY 3786 GAGATTATCGTCGACCAAGCGGCATCGTGCTCCCACTCTGCGATTGCGGGGCAATG 3845  
 DB 2450 ----- 2449  
 QY 3846 GATGCGCGATAGCGCTGCTGTTTCTCGGATGCGAGGATTTGCACTGCGCGTAGAA 3905  
 DB 2450 ----- 2449  
 QY 3906 CTTCCGAGGTGCTCCAGCTCAGGCAAGCAGTGAACCACTCGCGAGGGGATCGAGCCC 3965  
 DB 2450 ----- 2449  
 QY 3966 GGGGTGGCGAAGAACTCCAGCATGAGATCCCGCGCTGGAGGATCATCCAGCCGCGTTC 4025  
 DB 2450 ----- 2449  
 QY 4026 CCGGAAAAAGTTCGAAAGCCCAACCTTTTCATAGAAGCGCGGTGGGATCGAAATCTCG 4085  
 DB 2450 ----- 2449  
 QY 4086 TGATGGCAGGTTGGCGGTGCTGCTCGTTCATTTTGAACCCAGAGTCCCGCTCAGAAAG 4145  
 DB 2450 -----CGCTCAGAAAG 2459

XXII

QY 3006 TCACTCAAAGCGGTAAATACGGTTATCCACAGAAATCAGGGGATTAACGAGGAAAGAAAT 3065  
 Db 1712 TCACTCAAAGCGGTAAATACGGTTATCCACAGAAATCAGGGGATTAACGAGGAAAGAAAT 1771  
 QY 3066 GTGAGCAAAAGCCAGCAAAAGCCAGCAACCGTAAAAAGCCGGTTGCTGGCGTTTTT 3125  
 Db 1772 GTGAGCAAAAGCCAGCAAAAGCCAGCAACCGTAAAAAGCCGGTTGCTGGCGTTTTT 1831  
 QY 3126 CCATAGGCTCGCGCCCTGACAGCATCACAAAAATCGACGCTCAAGTCAGAGGTGGCG 3185  
 Db 1832 CCATAGGCTCGCGCCCTGACAGCATCACAAAAATCGACGCTCAAGTCAGAGGTGGCG 1891  
 QY 3186 AAAACCGACAGACTATAAAGATACAGCGGTTTCCCTCGGAAGCTCCCTCGTGGCGTC 3245  
 Db 1892 AAAACCGACAGACTATAAAGATACAGCGGTTTCCCTCGGAAGCTCCCTCGTGGCGTC 1951  
 QY 3246 TCCGTGTTCCGACCCCTGCGGCTTACGGATACCTGTCGCGCTTCTCCCTCGGGAAGGT 3305  
 Db 1952 TCCGTGTTCCGACCCCTGCGGCTTACGGATACCTGTCGCGCTTCTCCCTCGGGAAGGT 2011  
 QY 3306 GCGGCTTTCTCATAGCTACGCTGTAGTATCTCAGTTGCGTGTAGGTGCTTCGCTCAA 3365  
 Db 2012 GCGGCTTTCTCATAGCTACGCTGTAGTATCTCAGTTGCGTGTAGGTGCTTCGCTCAA 2071  
 QY 3366 GCTGGGCTGTGTCAAGAACCCCGCTTCAGCCGACCGCTGCGCTTATCCCGTAACTA 3425  
 Db 2072 GCTGGGCTGTGTCAAGAACCCCGCTTCAGCCGACCGCTGCGCTTATCCCGTAACTA 2131  
 QY 3426 TCGTCTTAGTCCAAACCCGTAAGACACGACTTATCGCCACTGSCACGACGCACTGGTAA 3485  
 Db 2132 TCGTCTTAGTCCAAACCCGTAAGACACGACTTATCGCCACTGSCACGACGCACTGGTAA 2191  
 QY 3486 CAGGATTAGCAGACGAGGTATGTAGCGGTGTACAGAGTTCTTGAAGTGTGGCTAA 3545  
 Db 2192 CAGGATTAGCAGACGAGGTATGTAGCGGTGTACAGAGTTCTTGAAGTGTGGCTAA 2251  
 QY 3546 CTACGGCTACACTAGAAAGACGATTTGGTATCTGGCTCTGCTGAGCGCATACCTT 3605  
 Db 2252 CTACGGCTACACTAGAAAGACGATTTGGTATCTGGCTCTGCTGAGCGCATACCTT 2311  
 QY 3606 CGAAAAAGAGTTGGTAGCTCTTGATCCGGCAACAAACACCGCTGGTAGCGGTGTTT 3665  
 Db 2312 CGAAAAAGAGTTGGTAGCTCTTGATCCGGCAACAAACACCGCTGGTAGCGGTGTTT 2371  
 QY 3666 TTTTGTGTCAGACGACAGATTACGGCGAGAAAAAGGATCTCAAGAGATCCTTTGAT 3725  
 Db 2372 TTTTGTGTCAGACGACAGATTACGGCGAGAAAAAGGATCTCAAGAGATCCTTTGAT 2431  
 QY 3726 CTTTCTACGGGTCTGACGCTCAGTGGGAACGAAACTCAGTTAAGGATTTTGTGAT 3785  
 Db 2432 CTTTCTACGGGTCTGAT 2449  
 QY 3786 GAGATTATCGTCCAGCAAGCGGCATCGTGCTCCCACTCCTGCACTTCGCGAGTTCCGGGCGATG 3845  
 Db 2450 2449  
 QY 3846 GATCGCGGATAGCGCTGCTGGTTCTGTGATGCGACGGATTTGCACTGCGGATAGAA 3905  
 Db 2450 2449  
 QY 3906 CTTCCGGAGGTCTCCAGCTCAGGACGAGCTGAACCACTCGCGAGGGATTCAGGCC 3965  
 Db 2450 2449  
 QY 3966 GGGGTGGCGAAGAACTCCAGCATGAGATCCCGCTGGAGGATCATCCAGCCGGGCTC 4025  
 Db 2450 2449  
 QY 4026 CCGGAAACGATTCCGAGCCCAACTTTTCAAGAGCGCGGTGGGAATCGAAATCTCG 4085  
 Db 2450 2449

QY 4086 TGATGECAGGTTGGCGCTCGCTTGGTGGTCAATTTTGAACCCAGAGTCCCCTCAGAG 4145  
 Db 2450 2459  
 QY 4146 AACTCGTCAAGAGCGGATAGAGCGGATGCGTCCGAATCGGAGCGCGCATCCGTAA 4205  
 Db 2460 AACTCGTCAAGAGCGGATAGAGCGGATGCGTCCGAATCGGAGCGCGCATCCGTAA 2519  
 QY 4206 AGCAGAGGAGCGGTAGCCCATTCGCGCAAGCTTTTCAGCAATATCAGGGTAGCC 4265  
 Db 2520 AGCAGAGGAGCGGTAGCCCATTCGCGCAAGCTTTTCAGCAATATCAGGGTAGCC 2579  
 QY 4266 AACCTATGTCTGATAGCGGTTCGCGCACACCCAGCGGCGCACAGTCGATCAATCCAGAA 4325  
 Db 2580 AACCTATGTCTGATAGCGGTTCGCGCACACCCAGCGGCGCACAGTCGATCAATCCAGAA 2639  
 QY 4326 AAGCGGCATTTTCCACCATGATATTGGCAAGCAGGATCGCCATGGGTCAACGACGAGA 4385  
 Db 2640 AAGCGGCATTTTCCACCATGATATTGGCAAGCAGGATCGCCATGGGTCAACGACGAGA 2699  
 QY 4386 TCCTCGCGCTCGGCGCATCGCGCTTTCAGCTTCGCGCAACAGTTTCGGCTGGCGGAGCCCC 4445  
 Db 2700 TCCTCGCGCTCGGCGCATCGCGCTTTCAGCTTCGCGCAACAGTTTCGGCTGGCGGAGCCCC 2759  
 QY 4446 TGATGCTCTTTCGTCAGATCATCTGATCGACAGACCGGCTTCCATCCGAGTAGTGCT 4505  
 Db 2760 TGATGCTCTTTCGTCAGATCATCTGATCGACAGACCGGCTTCCATCCGAGTAGTGCT 2819  
 QY 4506 CGCTCGATGCGATTTTCGCTTGGTTCGAATGGGCGAGGTAGCCGATCAAGCGTATGC 4565  
 Db 2820 CGCTCGATGCGATTTTCGCTTGGTTCGAATGGGCGAGGTAGCCGATCAAGCGTATGC 2879  
 QY 4566 AGCGCGCGCATTCGATCAGCATGATGATACCTTTCGCGAGAGCAAGTTCAGATGAC 4625  
 Db 2880 AGCGCGCGCATTCGATCAGCATGATGATACCTTTCGCGAGAGCAAGTTCAGATGAC 2939  
 QY 4626 AGGAGATCTCTGCCCCCGCACTTCGCCCAATAGCAGCGAGTCCCTTCGCGTTCAGTGACA 4685  
 Db 2940 AGGAGATCTCTGCCCCCGCACTTCGCCCAATAGCAGCGAGTCCCTTCGCGTTCAGTGACA 2999  
 QY 4686 ACCTCGACACAGCTCGCAAGGAAACCGCGTTCGTCGCGAGCGATAGCCGCGTGC 4745  
 Db 3000 ACCTCGACACAGCTCGCAAGGAAACCGCGTTCGTCGCGAGCGATAGCCGCGTGC 3059  
 QY 4746 TCGTCTCGAGTTCATTCAGGCGACCGGACAGGTTCGCTTCGCAAAAAAGAACCGGCGC 4805  
 Db 3060 TCGTCTCGAGTTCATTCAGGCGACCGGACAGGTTCGCTTCGCAAAAAAGAACCGGCGC 3119  
 QY 4806 CCCTGCGCTGACAGCGCGAACACCGCGCATCAGACGCGCATTCGTTGTTGCGCGAG 4865  
 Db 3120 CCCTGCGCTGACAGCGCGAACACCGCGCATCAGACGCGCATTCGTTGTTGCGCGAG 3179  
 QY 4866 TCATAGCGGAATAGCTCTCCACCAAGCGCGGAGAACCTGCGTGAATCATCTTGT 4925  
 Db 3180 TCATAGCGGAATAGCTCTCCACCAAGCGCGGAGAACCTGCGTGAATCATCTTGT 3239  
 QY 4926 TCAATCATGCGAAACGATCCTCATCTGCTTCGATCAGATTCCTGATCCCTTCGCGCAT 4985  
 Db 3240 TCAATCATGCGAAACGATCCTCATCTGCTTCGATCAGATTCCTGATCCCTTCGCGCAT 3299  
 QY 4986 CAGATCTTGGCGGCAAGAAAGCCATCCAGTTTACTTTGCGAGGCTTCCCAACCTTACCA 5045  
 Db 3300 CAGATCTTGGCGGCAAGAAAGCCATCCAGTTTACTTTGCGAGGCTTCCCAACCTTACCA 3359  
 QY 5046 GAGGCGCCCCAGGTGGCAATTCGCTTCGTTTCGATTAATAAACCGCCAGTCTAGC 5105  
 Db 3360 GAGGCGCCCCAGGTGGCAATTCGCTTCGTTTCGATTAATAAACCGCCAGTCTAGC 3419  
 QY 5106 TATCGCCATGTAAGCCCACTGCAAGCTACCTGCTTTCTCTT 5146  
 Db 3420 AACTGTTGGGAAGGCGGATCGGTGCGGCTCTTCGCTATT 3460





4025 CCGGAAACGATTCGAGAACCCAACTTTCATAGAGCGCGGTGGAATCGAAATCTCG 4085  
 2450 ----- 2449  
 4086 TGATGGCAGTTGGCGTCGCTGTGTCGATTCGAAACCCAGAGTCCCGCTCAGAG 4145  
 2450 -----CGTCAAG 2459  
 4146 AACTCGTCAAGAGGCGATAGAGGGATGCGCTCGGAATCGGGAGCGCGATACCGTAA 4205  
 2460 AACTCGTCAAGAGGCGATAGAGGGATGCGCTCGGAATCGGGAGCGCGATACCGTAA 2519  
 4206 AGCAGAGAGCGGTGAGCCCATTCGCGCAAGCTCTTCAGCAATATCAGGGTAGCC 4265  
 2520 AGCAGAGAGCGGTGAGCCCATTCGCGCAAGCTCTTCAGCAATATCAGGGTAGCC 2579  
 4266 AACGCTATGTCGTATAGCGGTGCGCCACACCCAGCGCGCACAGTCCGATGAATCCAGAA 4325  
 2580 AACGCTATGTCGTATAGCGGTGCGCCACACCCAGCGCGCACAGTCCGATGAATCCAGAA 2639  
 4326 AAGCGGCCATTTCCACCATGATATCGCAAGCAGGATCGCCATCGGTCACGACGAGA 4385  
 2640 AAGCGGCCATTTCCACCATGATATCGCAAGCAGGATCGCCATCGGTCACGACGAGA 2699  
 4386 TCCTCGCGGTGCGGCATCGCGCTTGAGCCTGCGGACAGTTCGGCTGGCGGAGCCCC 4445  
 2700 TCCTCGCGGTGCGGCATCGCGCTTGAGCCTGCGGACAGTTCGGCTGGCGGAGCCCC 2759  
 4446 TGATGCTCTTGTGTCAGATCATCTGATCGCAAGACCGGCTTCATCCGAGTACGTGCT 4505  
 2760 TGATGCTCTTGTGTCAGATCATCTGATCGCAAGACCGGCTTCATCCGAGTACGTGCT 2819  
 4506 CGCTCGATGCGATGTTTCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 4565  
 2820 CGCTCGATGCGATGTTTCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2879  
 4566 AGCGCGCGATGTCATCAGCATCATGATGATGATGATGATGATGATGATGATGATGATGAT 4625  
 2880 AGCGCGCGATGTCATCAGCATCATGATGATGATGATGATGATGATGATGATGATGATGAT 2939  
 4626 AGAGATCTTCCCGCGCATCTCGCCCAATAGCAGCCAGTCCCTTCCGCTTCAGTGACA 4685  
 2940 AGAGATCTTCCCGCGCATCTCGCCCAATAGCAGCCAGTCCCTTCCGCTTCAGTGACA 2999  
 4686 ACCTCGAGCACAGTCCGCGAGAACCCCGTGTGCGCCAGCCAGATGCGCGTGC 4745  
 3000 ACCTCGAGCACAGTCCGCGAGAACCCCGTGTGCGCCAGCCAGATGCGCGTGC 3059  
 4746 TCCTCTGTCAGTTCAITTCAGGGCACCGGACAGTTCGCTGTTGACAAAAGAACCGGGCGC 4805  
 3060 TCCTCTGTCAGTTCAITTCAGGGCACCGGACAGTTCGCTGTTGACAAAAGAACCGGGCGC 3119  
 4806 CCTGCGCTGACAGCGGACACCGGCGCATCAGACGCGGATGCTGCTGCTGCTGCTGCTGCT 4865  
 3120 CCTGCGCTGACAGCGGACACCGGCGCATCAGACGCGGATGCTGCTGCTGCTGCTGCTGCT 3179  
 4866 TCATAGCCGAATAGCTCTCCACCCAGCGCGGACACCTGCGTCAATCCATCTTGT 4925  
 3180 TCATAGCCGAATAGCTCTCCACCCAGCGCGGACACCTGCGTCAATCCATCTTGT 3239  
 4926 TCAATCATCGAAAGATCT 4985  
 3240 TCAATCATCGAAAGATCT 3299  
 4986 CAGATCTTGGCGGCAAGAAAGCCATCCAGTTTACTTTGACGGGCTTCCCAACCTTACCA 5045  
 3300 CAGATCTTGGCGGCAAGAAAGCCATCCAGTTTACTTTGACGGGCTTCCCAACCTTACCA 3359  
 5046 GAGGCGCGCCAGCTGGCAATTCGGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 5105  
 3360 GAGGCGCGCCAGCTGGCAATTCGGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3419  
 5106 TATCGCCATGTAAGCCCACTGCAAGCTACCTGCTTCTCTT 5146

Db 3420 AACTGTTGGAGGCGCATCGGTGCGGCTCTTCGCTATT 3460

RESULT 13  
 AAL62059

ID AAL62059 standard; DNA; 3534 BP.

XX AAL62059;

DT 22-SEP-2003 (first entry)

XX TI-GHRH plasmid DNA.

Plasmid-mediated supplementation; anaemia; tumour; adenoma; melanoma;  
 sarcoma; immune dysfunction; carcinoma; leukaemia; kidney failure;  
 lymphoma; weight loss; lymphopoesis; appetite stimulant; anorectic;  
 growth hormone releasing hormone; GHRH; cyclic; circular; gene; ds.

OS Unidentified.

XX WO2003049700-A2.

XX 19-JUN-2003.

XX 10-DEC-2002; 2002WO-US039509.

XX 11-DEC-2001; 2001US-0339610P.

XX (ADVI-) ADVISYS INC.

XX (BAYU) BAYLOR COLLEGE MEDICINE.

XX Draghia-Akli R, Carpenter RH, Kern DR, Schwartz RJ, King G;  
 Hahn K, Brenner MK;

XX WPI; 2003-558968/52.

Treating anemia, immune dysfunction, tumor, increasing total red blood  
 cell mass, reversing wasting or abnormal weight loss in subject, by  
 administering nucleic acid construct encoding growth-hormone-releasing-  
 hormone.

Claim 4; Page 191-193; 212pp; English.

The invention relates to compositions and methods for plasmid-mediated  
 supplementation. The method is useful for treating anaemia, tumour (such  
 as adenoma, mast cell tumour, melanoma, sarcoma or solid tumour), immune  
 dysfunction, carcinoma (benign or malignant), leukaemia, lymphoma or  
 kidney failure, for preventing the development of metastatic tumour, for  
 increasing total red blood cell mass, for reversing wasting, abnormal  
 weight loss or suppression of lymphopoesis, in a subject, or for  
 increasing weight gain in a chronically ill subject or, or for extending  
 life expectancy for a chronically ill subject. The present sequence is TI  
 -growth hormone releasing hormone (GHRH) plasmid DNA. This sequence is  
 used to illustrate the method of the invention

SQ Sequence 3534 BP; 764 A; 1017 C; 978 G; 775 T; 0 U; 0 Other;

Query Match 30.4%; Score 1603.8; DB 8; Length 3534;

Best Local Similarity 82.8%; Pred. No. 1.8e-234;

Matches 2022; Conservative 0; Mismatches 27; Indels 392; Gaps 1;

QY 2706 CTAGACGTAATCATGCTATAGCTGTTCTCTGTGAAATTTATCCGCTCACAAATCC 2765

Db 1412 CTGCGGTAATCATGCTATAGCTGTTCTCTGTGAAATTTATCCGCTCACAAATCC 1471

QY 2766 ACACAACATACGAGCGGAAGCATAAAGTGAAGCCTGGGTGCTTAATGAGTGA 2825

Db 1472 ACACAACATACGAGCGGAAGCATAAAGTGAAGCCTGGGTGCTTAATGAGTGA 1531

QY 2826 ACTCACATTAATTCGTTGCGCTCACTCCCGCTTTCAGTCCGGAAACCTGTCGTGCA 2885

Db 1532 ACTCACATTAATTCGTTGCGCTCACTCCCGCTTTCAGTCCGGAAACCTGTCGTGCA 1591

3966	GGGTGGCGCGAAGAACTCCAGCATGAGATCCCGCGCTGGAGGATCATCCAGCGCGCTC	4025
2450	-----	2449
4026	CCGAAAACGATTCCGAAGCCCAACCTTTATAGAAGCGCGGTGGAATCGAAATCTCG	4085
2450	-----	2449
4086	TGATGCGAGGTTGGCGCTCGCTTGTGCTGCTCATTTTCGAACCCAGAGTCCCGCTCAGAAG	4145
2450	-----	2459
4146	AACTCCTCAAGAAGCGATAGAAGCGATCGCTCGAATCGGAGCGCGATACGTAAC	4205
2460	AACTCCTCAAGAAGCGATAGAAGCGATCGCTCGAATCGGAGCGCGATACGTAAC	2519
4206	AGCAGAGAGCGGTGAGCCCATTCGCGCCAAAGCTTTTCAGCAATATCAGCGGTAGCC	4265
2520	AGCAGAGAGCGGTGAGCCCATTCGCGCCAAAGCTTTTCAGCAATATCAGCGGTAGCC	2579
4266	AACGCTATGCTCTGATAGCGTCCGCGCCACACCGCGCGCCACAGTCTGATGATTCAGAA	4325
2580	AACGCTATGCTCTGATAGCGTCCGCGCCACACCGCGCGCCACAGTCTGATGATTCAGAA	2639
4326	AAGCGGCCATTTTCCACCATGATATTCGCAAGCAGGCGATCGCATGATTCAGAGAG	4385
2640	AAGCGGCCATTTTCCACCATGATATTCGCAAGCAGGCGATCGCATGATTCAGAGAG	2699
4386	TCCTCGCGCTCGGCGATGCGCGCTTTCAGCTTGGCGAAAGCTTTCGCGCTCGCGCGCGCC	4445
2700	TCCTCGCGCTCGGCGATGCGCGCTTTCAGCTTGGCGAAAGCTTTCGCGCTCGCGCGCGCC	2759
4446	TGATGCTCTTCGTCAGAGATCATCTGATCGCAAGACCGGCTTTCATTCGAGTACGTC	4505
2760	TGATGCTCTTCGTCAGAGATCATCTGATCGCAAGACCGGCTTTCATTCGAGTACGTC	2819
4506	CGCTCGATGCGATGTTTCGCTTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGT	4565
2820	CGCTCGATGCGATGTTTCGCTTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGT	2879
4566	AGCGCGGATTCGATCAGCGATGATGATGATGATGATGATGATGATGATGATGATGAT	4625
2880	AGCGCGGATTCGATCAGCGATGATGATGATGATGATGATGATGATGATGATGATGAT	2939
4626	AGGAGATCTTCGCGCGCATCTTCGCCAATAGCAGCGCGCTTCGCTTCGCTTCGCTTC	4685
2940	AGGAGATCTTCGCGCGCATCTTCGCCAATAGCAGCGCGCTTCGCTTCGCTTCGCTTC	2999
4686	ACGTCGAGCAGCTGCGCAAGAAACCGCGCTCGTGGCGCAGCGCGATAGCGCGCTGCC	4745
3000	ACGTCGAGCAGCTGCGCAAGAAACCGCGCTCGTGGCGCAGCGCGATAGCGCGCTGCC	3059
4746	TCGTCCTGCGATTCATTCAGCGCACCGGACAGGTCGCTTTCGCAAAAGAACCGCGCGC	4805
3060	TCGTCCTGCGATTCATTCAGCGCACCGGACAGGTCGCTTTCGCAAAAGAACCGCGCGC	3119
4806	CCCTGCGCTGACAGCGCGCAACACCGCGCGCATCAGAGAGCGGATGCTGTTGTCGCG	4865
3120	CCCTGCGCTGACAGCGCGCAACACCGCGCGCATCAGAGAGCGGATGCTGTTGTCGCG	3179
4866	TCATAGCGGATGAGCTTCACCGCAGCGCGCGGAGAACCTGGTGGCAATCCATCTTGT	4925
3180	TCATAGCGGATGAGCTTCACCGCAGCGCGCGGAGAACCTGGTGGCAATCCATCTTGT	3239
4926	TCATATCGGAAACGATCTTCATCTCTCTTTCATCAGATCTTCATCTTCCTCGCGCAT	4985
3240	TCATATCGGAAACGATCTTCATCTCTCTTTCATCAGATCTTCATCTTCCTCGCGCAT	3299
4986	CAGATCTTCGCGCAAGAAAGCAATCCAGTTTACTTTGACAGGCTTCCCAACCTTACCA	5045
3300	CAGATCTTCGCGCAAGAAAGCAATCCAGTTTACTTTGACAGGCTTCCCAACCTTACCA	3359
5046	GAGGCGCGCGCGAGTGGCAATTCGCTTTCGCTTTCATATAAAACCGCGCGCTAGC	5105
2886	GCTCATTAATGAATCGGCCAACCGCGCGGAGAGCGGTTTTCGTAATTCGCGCTCTTC	2945
1592	GCTCATTAATGAATCGGCCAACCGCGCGGAGAGCGGTTTTCGTAATTCGCGCTCTTC	1651
2946	CGCTTCCTCGCTACTGACTCGCTCGCTCGCTCGCTCGCTCGCTCGCTCGCTCGCTCG	3005
1652	CGCTTCCTCGCTACTGACTCGCTCGCTCGCTCGCTCGCTCGCTCGCTCGCTCGCTCG	1711
3006	TCATCAAGAGGCTTAATACGTTATCCACAGATCAGGGATACGAGGAGGATACAG	3065
1712	TCATCAAGAGGCTTAATACGTTATCCACAGATCAGGGATACGAGGAGGATACAG	1771
3066	GTGACAAAAGCCAGCAAAAGCCAGGAACCGTAAAGCCGCGTTCGCTGCGCTTTT	3125
1772	GTGACAAAAGCCAGCAAAAGCCAGGAACCGTAAAGCCGCGTTCGCTGCGCTTTT	1831
3126	CCATAGGCTTCGCGCCCTGACAGCATCACAAAATCGACGCTCAAGTCAGAGTGGCG	3185
1832	CCATAGGCTTCGCGCCCTGACAGCATCACAAAATCGACGCTCAAGTCAGAGTGGCG	1891
3186	AAACCGCAGGACTATAAAGATACAGAGCTTTCGCGCTTTCGCGCTTTCGCGCTTTC	3245
1892	AAACCGCAGGACTATAAAGATACAGAGCTTTCGCGCTTTCGCGCTTTCGCGCTTTC	1951
3246	TCCTGTTCCGACCTCGCGCTTACCGGATACCTGTCGCGCTTTCGCGCTTTCGCGGAGCG	3305
1952	TCCTGTTCCGACCTCGCGCTTACCGGATACCTGTCGCGCTTTCGCGCTTTCGCGGAGCG	2011
3306	GGCGCTTTCATAGCTCAGCTGTAGTATCTCAGTTCGCTGAGTTCGCTGCTCCAA	3365
2012	GGCGCTTTCATAGCTCAGCTGTAGTATCTCAGTTCGCTGAGTTCGCTGCTCCAA	2071
3366	GCTGGCTGTGTCAGCAACCCCGTTTCAGCGCGCGCTTCGCGCTTTCGCGTAACTA	3425
2072	GCTGGCTGTGTCAGCAACCCCGTTTCAGCGCGCGCTTCGCGCTTTCGCGTAACTA	2131
3426	TCGCTTTGAGTCCAAACCGGTAAAGACAGCTTATCGCCATCGCGCAGCGCTGCTAA	3485
2132	TCGCTTTGAGTCCAAACCGGTAAAGACAGCTTATCGCCATCGCGCAGCGCTGCTAA	2191
3486	CAGGATTCAGAGCGAGGATGATGAGCGGCTGCTACAGAGTTCCTGAAAGTGGTGGCTAA	3545
2192	CAGGATTCAGAGCGAGGATGATGAGCGGCTGCTACAGAGTTCCTGAAAGTGGTGGCTAA	2251
3546	CTAGGCTACACTAGAAAGACAGTATTTGGTATCTGGGCTCTGCTGAAGCCAGTTACCT	3605
2252	CTAGGCTACACTAGAAAGACAGTATTTGGTATCTGGGCTCTGCTGAAGCCAGTTACCT	2311
3606	CGGAAAAGAGTTGGTAGCTTCGATCGGCAAAACAAACCGCTGCTGAGCGGCTGTT	3665
2312	CGGAAAAGAGTTGGTAGCTTCGATCGGCAAAACAAACCGCTGCTGAGCGGCTGTT	2371
3666	TTTTGTTTGAAGCAGAGATTCGCGCAGAAAGAGATCTCAAGAGATCTCTTTGAT	3725
2372	TTTTGTTTGAAGCAGAGATTCGCGCAGAAAGAGATCTCAAGAGATCTCTTTGAT	2431
3726	CTTTTCTACGCGGCTGAGCGCTCAGTGGAACGAAATCACTGAGGATTTTGGTAT	3785
2432	CTTTTCTACGCGGCTGAGCGCTCAGTGGAACGAAATCACTGAGGATTTTGGTAT	2449
3786	GAGATATCTGTCGACCAAGGCGCATCGTGCCTCCCGCTTCCTGAGTTCGGGGCATG	3845
2450	-----	2449
3846	GATGCGGATAGCGCTGCTGTTTCCTGATGCGGAGGATTCGACTGCGCGTGAAG	3905
2450	-----	2449
3906	CTCCGCGAGTCTCCAGCTCAGGAGAGTGAACCACTCGCGAGGGATTCAGGCC	3965
2450	-----	2449

Db 3360 GAGGCGCCAGCTGCGCAATTCGGTTTCGTTGCTGTGCTCAATAAACCCGCGCTAGC 3419  
 QY 5106 TATCGCATGTAAAGCCCACTGCAAGCTACTGCTTCTCTT 5146  
 Db 3420 AACTGTGGGAAGGCGATCGGTGCGGCTCTTCGCTATT 3460

RESULT 14  
 AAL62058  
 ID AAL62058 standard; DNA; 3534 BP.  
 AC AAL62058;  
 XX  
 DT 22-SEP-2003 (first entry)  
 DE PSP-HV-GHRH plasmid DNA.  
 XX  
 KW Plasmid-mediated supplementation; anaemia; tumour; adenoma; melanoma;  
 KW sarcoma; immune dysfunction; carcinoma; leukaemia; kidney failure;  
 KW lymphoma; weight loss; lymphopoesis; appetite stimulant; anorectic;  
 KW growth hormone releasing hormone; GHRH; cyclic; circular; gene; ds.  
 XX  
 OS Unidentified.  
 XX  
 PN WO2003049700-A2.  
 XX  
 PD 19-JUN-2003.  
 XX  
 PF 10-DEC-2002; 2002WO-US039509.  
 XX  
 PR 11-DEC-2001; 2001US-0339610P.  
 XX  
 PA (ADVI-) ADVISYS INC.  
 PA (BAYU) BAYLOR COLLEGE MEDICINE.  
 XX  
 XX Draghia-Akli R, Carpenter RH, Kern DR, Schwartz RJ, King G;  
 PI Hahn K, Brenner MK;  
 PI  
 XX WPI; 2003-558968/52.  
 XX  
 PT Treating anemia, immune dysfunction, tumor, increasing total red blood  
 PT cell mass, reversing wasting or abnormal weight loss in subject, by  
 PT administering nucleic acid construct encoding growth-hormone-releasing-  
 PT hormone.  
 XX  
 PS Claim 4; Page 189-191; 212pp; English.  
 XX  
 CC The invention relates to compositions and methods for plasmid-mediated  
 CC supplementation. The method is useful for treating anaemia, tumour (such  
 CC as adenoma, mast cell tumour, melanoma, sarcoma or solid tumour), immune  
 CC dysfunction, carcinoma (benign or malignant), leukaemia, lymphoma or  
 CC kidney failure, for preventing the development of metastatic tumour, for  
 CC increasing total red blood cell mass, for reversing wasting, abnormal  
 CC weight loss or suppression of lymphopoesis, in a subject, or for  
 CC increasing weight gain in a chronically ill subject, or for extending  
 CC life expectancy for a chronically ill subject. The present sequence is  
 CC PSP-HV-growth hormone releasing hormone (GHRH) plasmid DNA. This sequence  
 CC is used to illustrate the method of the invention  
 XX  
 SQ Sequence 3534 BP; 764 A; 1018 C; 979 G; 773 T; 0 U; 0 Other;

Query Match 30.4%; Score 1603.8; DB 8; Length 3534;  
 Best Local Similarity 82.8%; Pred. No. 1.8e-234;  
 Matches 2022; Conservative 0; Mismatches 27; Indels 392; Gaps 1;

QY 2706 CTAGACGTAAATCATGTATAGTGTTCCTGTGTGAATTTGTTATCCCTCACAAATTC 2765  
 Db 1412 CTGGGTAAATCATGTATAGTGTTCCTGTGTGAATTTGTTATCCCTCACAAATTC 1471  
 QY 2766 ACACAACTACGAGCGGGAAGCATAAAGTGAAGCCCTGGGTGCTTAATGATGAGCTA 2825  
 Db 1472 ACACAACTACGAGCGGGAAGCATAAAGTGAAGCCCTGGGTGCTTAATGATGAGCTA 1531

QY 2826 ACTCATTAAATGCGTTGCGCTCACTGCCCGTTTCCAGTGGGAAACCTGTCGTGCCA 2885  
 Db 1532 ACTCATTAAATGCGTTGCGCTCACTGCCCGTTTCCAGTGGGAAACCTGTCGTGCCA 1591  
 QY 2886 GCTGATTAAATGAAATCGGCAACGCGGGGAGAGCGGTTTGGCTATTTGGGGGCTTTC 2945  
 Db 1592 GCTGATTAAATGAAATCGGCAACGCGGGGAGAGCGGTTTGGCTATTTGGGGGCTTTC 1651  
 QY 2946 CGCTTCCTCGCTCACTGCTGCGTTCGCTGCGTTCGCTGCGGCGAGCGGTATCAGC 3005  
 Db 1652 CGCTTCCTCGCTCACTGCTGCGTTCGCTGCGTTCGCTGCGGCGAGCGGTATCAGC 1711  
 QY 3006 TCACTCAAAGGCGTAATACGGTTTATCCACAGATCAGGGGATACCGAGGAAAGAAAT 3065  
 Db 1712 TCACTCAAAGGCGTAATACGGTTTATCCACAGATCAGGGGATACCGAGGAAAGAAAT 1771  
 QY 3066 GTGAGCAAAAGGCCAGCAAAAGGCCAGCAACCGTAAAGAGCCGCTTCTGGCGTTT 3125  
 Db 1772 GTGAGCAAAAGGCCAGCAAAAGGCCAGCAACCGTAAAGAGCCGCTTCTGGCGTTT 1831  
 QY 3126 CCATAGGCTCCGCCCTCGCTGACGAGCATACAAAATACGAGCTCAAGTCAGAGTGCG 3185  
 Db 1832 CCATAGGCTCCGCCCTCGCTGACGAGCATACAAAATACGAGCTCAAGTCAGAGTGCG 1891  
 QY 3186 AAACCCGACAGGACTATAAGATACAGGCGTTTCCCTCGGAAGCTCCCTCGTGCGTC 3245  
 Db 1892 AAACCCGACAGGACTATAAGATACAGGCGTTTCCCTCGGAAGCTCCCTCGTGCGTC 1951  
 QY 3246 TCCTGTTCCGACCTCGCGCTTACCGGATACCTGCGGATACCTGCGGCTTCTCCCTCGG 2011  
 Db 1952 TCCTGTTCCGACCTCGCGCTTACCGGATACCTGCGGATACCTGCGGCTTCTCCCTCGG 2071  
 QY 3306 GCGCTTCTCATAGCTCAAGCTAGCTATCTCAGTTGCGTGTAGTGTGCTGCTCA 3365  
 Db 2012 GCGCTTCTCATAGCTCAAGCTAGCTATCTCAGTTGCGTGTAGTGTGCTGCTCA 2071  
 QY 3366 GCTGGGCTGTGCGACGAAACCCCGCTTACGCGGAGCCGCTGCGCTTATCCGTA 3425  
 Db 2072 GCTGGGCTGTGCGACGAAACCCCGCTTACGCGGAGCCGCTGCGCTTATCCGTA 2131  
 QY 3426 TCGTCTTGTAGTCAACCCCGCTTACGCGGAGCCGCTGCGCTTATCCGTA 3485  
 Db 2132 TCGTCTTGTAGTCAACCCCGCTTACGCGGAGCCGCTGCGCTTATCCGTA 2191  
 QY 3486 CAGATTAGCAGAGGAGTATGAGCGGTGTACAGAGTTCTTGAAGTGGTGGCTAA 3545  
 Db 2192 CAGATTAGCAGAGGAGTATGAGCGGTGTACAGAGTTCTTGAAGTGGTGGCTAA 2251  
 QY 3546 CTACGGCTACCTAGAGAACAGTATTTGGTATCTGCGCTCTGCTGAGCGAGTTACCTT 3605  
 Db 2252 CTACGGCTACCTAGAGAACAGTATTTGGTATCTGCGCTCTGCTGAGCGAGTTACCTT 2311  
 QY 3606 CGGAAAGAGTGTGTAGCTCTTGTATCCGCAAAACAAACCCGCTGAGCGGTGTT 3665  
 Db 2312 CGGAAAGAGTGTGTAGCTCTTGTATCCGCAAAACAAACCCGCTGAGCGGTGTT 2371  
 QY 3666 TTTTGTTCAGAGCAGCAGATTACGCGCAGAAAAAAGGATCTCAAGAGATCTTTGAT 3725  
 Db 2372 TTTTGTTCAGAGCAGCAGATTACGCGCAGAAAAAAGGATCTCAAGAGATCTTTGAT 2431  
 QY 3726 CTTTCTACGGGCTGTGAGCTCAGTGGNACGAAACTCACGTTAAGGATTTTGGTCA 3785  
 Db 2432 CTTTCTACGGGCTGTGAGCTCAGTGGNACGAAACTCACGTTAAGGATTTTGGTCA 2449  
 QY 3786 GAGATTATGTCGACCAAGAGCGGCATCGTGCTCCCACTCTCTGAGTTTCGGGCGATG 3845  
 Db 2450 ----- 2449  
 QY 3846 GATGCGGATAGCCGCTGCTGGTTTCTGGATGCCAGGATTTGCACTGCGCGTAGAA 3905  
 Db 2450 ----- 2449

Db	3300	CAGATCCTTGGCGCGAAGAAAGCATCCAGTTTACATTTGCGGGCTTCCCAACCTTACCA	3355
Qy	5046	GAGGGGCGCCAGCTGGCAATTCGGTTGCTTGCCTTGCATATAAACCCGCCAGTCTAGC	5105
Db	3360	GAGGGCGCCAGCTGGCAATTCGGTTGCTTGCCTTGCATATAAACCCGCCAGTCTAGC	3419
Qy	5106	TATGCCATGTAAAGCCCACTGCAAGCTACCTGCTTCTCTT	5146
Db	3420	AACTGTTGGGAAGGGCGATCGGTGCGGGCCCTCTTCGCTATT	3460
RESULT 15			
AAAL62061	AAL62061 standard; DNA; 3534 BP.		
XX	AC	AAAL62061;	
XX	DT	22-SEP-2003 (first entry)	
XX	DE	15/27/28-GHRH plasmid DNA.	
XX	XX	Plasmid-mediated supplementation; anaemia; tumour; adenoma; melanoma;	
KW	KW	sarcoma; immune dysfunction; carcinoma; leukaemia; kidney failure;	
KW	KW	lymphoma; weight loss; lymphoepoiesis; appetite stimulant; anorectic;	
KW	KW	growth hormone releasing hormone; GHRH; cyclic; circular; gene; ds.	
XX	OS	Unidentified.	
XX	OS	WO2003049700-A2.	
PN	PN	19-JUN-2003.	
XX	PD		
XX	XX	10-DEC-2002; 2002WO-US039509.	
PF	PF		
XX	XX	11-DEC-2001; 2001US-0339610P.	
PR	PR	(ADVI-) ADVISYS INC.	
XX	PA	(BAYU) BAYLOR COLLEGE MEDICINE.	
XX	PI	Draghia-Akli R, Carpenter RH, Kern DR, Schwartz RJ, King G;	
PI	PI	Hahn K, Brenner MK;	
XX	XX	WPI; 2003-558968/52.	
DR	DR		
XX	XX	Treating anemia, immune dysfunction, tumor, increasing total red blood	
PT	PT	cell mass, reversing wasting or abnormal weight loss in subject, by	
PT	PT	administering nucleic acid construct encoding growth-hormone-releasing-	
PT	PT	hormone.	
XX	XX	Claim 4; Page 196-197; 212pp; English.	
PS	PS		
XX	XX	The invention relates to compositions and methods for plasmid-mediated	
CC	CC	supplementation. The method is useful for treating anaemia, tumour (such	
CC	CC	as adenoma, mast cell tumour, melanoma, sarcoma or solid tumour), immune	
CC	CC	dysfunction, carcinoma (benign or malignant), leukaemia, lymphoma or	
CC	CC	kidney failure, for preventing the development of metastatic tumour, for	
CC	CC	increasing total red blood cell mass, for reversing wasting, abnormal	
CC	CC	weight loss or suppression of lymphopoiesis, in a subject, or for	
CC	CC	increasing weight gain in a chronically ill subject or, or for extending	
CC	CC	life expectancy for a chronically ill subject. The present sequence is	
CC	CC	15/27/28-growth hormone releasing hormone (GHRH) plasmid DNA. This	
CC	CC	sequence is used to illustrate the method of the invention	
XX	XX		
XX	XX	Sequence 3534 BP; 764 A; 1017 C; 978 G; 775 T; 0 U; 0 Other;	
SQ	SQ		
Query Match			
Best Local Similarity 30.4%; Score 1603.8; DB 8; Length 3534;			
Matches 2022; Conservative 82.8%; Pred. No. 1.8e-234; Indels 392; Gaps			
1			
Qy	2706	CTAGACGTATCATGGTCATAGCTGTTTCTGTGTGAAATGTTATCCGCTCAATCC	2768
Db	1412	CTTGGCGTAATCATGGTCATAGCTGTTTCTGTGTGAAATGTTATCCGCTCAATCC	1419

QY	2766	ACACAACATACGAGCGGGAAGCATAAAGTGTAAAGCTCGGGTGCTTAAGAGTGAGCTTA	2825
Db	1472	ACACAACATACGAGCGGGAAGCATAAAGTGTAAAGCTCGGGTGCTTAAGAGTGAGCTTA	1531
QY	2826	ACTCATTAAATGCGTTCGCTCACTGCGCCCTTTCCAGTCGGGAACCTTCGTGCGCA	2885
Db	1532	ACTCATTAAATGCGTTCGCTCACTGCGCCCTTTCCAGTCGGGAACCTTCGTGCGCA	1591
QY	2886	GCTGCATTAAATGCGTTCGCTCACTGCGCCCTTTCCAGTCGGGAACCTTCGTGCGCA	2945
Db	1592	GCTGCATTAAATGCGTTCGCTCACTGCGCCCTTTCCAGTCGGGAACCTTCGTGCGCA	1651
QY	2946	CGCTTCCTCGCTCACTGCTCGCTCGCTCGCTCGCTCGCTCGCTCGCTCGCTCGCT	3005
Db	1652	CGCTTCCTCGCTCACTGCTCGCTCGCTCGCTCGCTCGCTCGCTCGCTCGCTCGCT	1711
QY	3006	TCACCTCAAAGCGGTAAATACCGTTCATCCACAGAAATCAGGGGATTAACGACAGGAAGAACAT	3065
Db	1712	TCACCTCAAAGCGGTAAATACCGTTCATCCACAGAAATCAGGGGATTAACGACAGGAAGAACAT	1771
QY	3066	GTGAGCAAAAGGCCAGCAAAAGGCCAGGAACCGTAAAAAGCCCGTTGCTGGCGTTTTT	3125
Db	1772	GTGAGCAAAAGGCCAGCAAAAGGCCAGGAACCGTAAAAAGCCCGTTGCTGGCGTTTTT	1831
QY	3126	CCATAGGCTCGCCCGCCCTGACGAGCATCAAAATTCGAGCTCAAGTCAAGGTGGCG	3185
Db	1832	CCATAGGCTCGCCCGCCCTGACGAGCATCAAAATTCGAGCTCAAGTCAAGGTGGCG	1891
QY	3186	AAACCCGACAGGACTATAAAGATACCAAGCGGTTCGCCCTTGAAGTCCCTCGTGGCGCTC	3245
Db	1892	AAACCCGACAGGACTATAAAGATACCAAGCGGTTCGCCCTTGAAGTCCCTCGTGGCGCTC	1951
QY	3246	TCCGTGTCGACACCTGCGCTTACCGGATACCTGTCGCGCTTTCTCCCTTCGGGAAGCGT	3305
Db	1952	TCCGTGTCGACACCTGCGCTTACCGGATACCTGTCGCGCTTTCTCCCTTCGGGAAGCGT	2011
QY	3306	GGCGCTTTCTCATAGCTACGCTGTAGTATCTCAGTTCGCTGAGTGTGCTGCTCCAA	3365
Db	2012	GGCGCTTTCTCATAGCTACGCTGTAGTATCTCAGTTCGCTGAGTGTGCTGCTCCAA	2071
QY	3366	GCTGGGCTGTGTGACGAAACCCCGCTTACGCGGACCGCTGCGCTTATCCCGTAACTA	3425
Db	2072	GCTGGGCTGTGTGACGAAACCCCGCTTACGCGGACCGCTGCGCTTATCCCGTAACTA	2131
QY	3426	TCGTCTTGAGTCCAAACCGGTAAAGACGACTTATCGCCACTGGCAGCAGCCACTGGTAA	3485
Db	2132	TCGTCTTGAGTCCAAACCGGTAAAGACGACTTATCGCCACTGGCAGCAGCCACTGGTAA	2191
QY	3486	CAGGATTTAGCAGAGCGGTATGTAGCGGTGCTACAGAGTCTTGAAGTGTGGCGTAA	3545
Db	2192	CAGGATTTAGCAGAGCGGTATGTAGCGGTGCTACAGAGTCTTGAAGTGTGGCGTAA	2251
QY	3546	CTACGGCTACACTAGAAAGACGATTTTGGTATCTGCGCTCTGCTGAAGCCAGTTACCTT	3605
Db	2252	CTACGGCTACACTAGAAAGACGATTTTGGTATCTGCGCTCTGCTGAAGCCAGTTACCTT	2311
QY	3606	CGGAAAAAGATTGGTAGCTCTTGATCCGCGCAAAACAAACCGCTGTGAGCGGTGGTTT	3665
Db	2312	CGGAAAAAGATTGGTAGCTCTTGATCCGCGCAAAACAAACCGCTGTGAGCGGTGGTTT	2371
QY	3666	TTTTTGTTCAGAGCAGCAGATTACCGCGCAAAAGAAAGATCTCAAGAGATCTTTGAT	3725
Db	2372	TTTTTGTTCAGAGCAGCAGATTACCGCGCAAAAGAAAGATCTCAAGAGATCTTTGAT	2431
QY	3726	CTTTCTACGGGTCTGACGCTCAGTGGAAACGAAACCTCACGTTAAGGGATTTCGTCA	3785
Db	2432	CTTTCTACGGGTCTGACGCTCAGTGGAAACGAAACCTCACGTTAAGGGATTTCGTCA	2449
QY	3786	GAGATTATCGTCACAAAGCGGCATCGTGCTCCCACTCTCTGAGTTCGGGGCATG	3845
Db	2450	-----	2449

QY	3846	GATGCGCGATAGCCGCTGCTGTTTCTGTGATGCGACGGAATTTGCACTGCGCGTAGAA	3905
Db	2450	-----	2449
QY	3906	CTCCGCGAGGTGCTCCAGCCTCAGGCGAGCTGAACCAACTCGCGAGGGATCGAGCCC	3965
Db	2450	-----	2449
QY	3966	GGGTGGCGGAAGAACTCCAGCATGAGATCCCGCGCTGGAGGATCATCCAGCCGGCGTC	4025
Db	2450	-----	2449
QY	4026	CCGAAAAACGATTCCGAAGCCCAACTTTTATAGAAAGCGCGGTGGAAATCGAAATCTCG	4085
Db	2450	-----	2449
QY	4086	TGATGGCAGGTTGGGCGTTCGTTGGTCCGTCATTTTGAACCCCGAGTCCCGCTCAGAAG	4145
Db	2450	-----	2449
QY	4146	AACTCGTCAGAAAGCGGATAGAAAGCGGATGCGTCGGAATCGGAGCGGCGATACCGTAA	4205
Db	2460	AACTCGTCAGAAAGCGGATAGAAAGCGGATGCGTCGGAATCGGAGCGGCGATACCGTAA	2519
QY	4206	AGCACGAGGAAGCGGTGAGCCCATTCGCGCCCAAGCTCTTCAGCAATATCAAGGTAGCC	4265
Db	2520	AGCACGAGGAAGCGGTGAGCCCATTCGCGCCCAAGCTCTTCAGCAATATCAAGGTAGCC	2579
QY	4266	AACTGATGCTGCTGATAGCGGTCCGCCACACCCAGCGCGGCACAGTCGATGAATCCAGAA	4325
Db	2580	AACTGATGCTGCTGATAGCGGTCCGCCACACCCAGCGCGGCACAGTCGATGAATCCAGAA	2639
QY	4326	AAAGCGCATTTTCCACCATGATATTCGGAAGCAGGATTCGCATCGGTCACGACGAGA	4385
Db	2640	AAAGCGCATTTTCCACCATGATATTCGGAAGCAGGATTCGCATCGGTCACGACGAGA	2699
QY	4386	TCCTCGCGCTCGCGCATTCGCGCTTGAGCTTGCGCAACAGTTCGCTGGCGAGAGCCCC	4445
Db	2700	TCCTCGCGCTCGCGCATTCGCGCTTGAGCTTGCGCAACAGTTCGCTGGCGAGAGCCCC	2759
QY	4446	TGATGCTTCTGCTCCAGATCATCTGATCGACAAAGACCGGCTTCCATCCGAGTACGTGCT	4505
Db	2760	TGATGCTTCTGCTCCAGATCATCTGATCGACAAAGACCGGCTTCCATCCGAGTACGTGCT	2819
QY	4506	CGCTCGATCGATGTTTTCGCTTGGTTCGAAATGGCGAGTACCGGATCAAGCGTATGC	4565
Db	2820	CGCTCGATCGATGTTTTCGCTTGGTTCGAAATGGCGAGTACCGGATCAAGCGTATGC	2879
QY	4566	AGCGCGCATTTGCTCAGCATCAGCCATGATGGATCTTCTCGCGAGGACCAAGGTGAGATGAC	4625
Db	2880	AGCGCGCATTTGCTCAGCATCAGCCATGATGGATCTTCTCGCGAGGACCAAGGTGAGATGAC	2939
QY	4626	AGGAGATCTTGGCCCGGCTTCGCGCCCAATAGCAGCAGTCCCTTCCCGCTTCAGTGACA	4685
Db	2940	AGGAGATCTTGGCCCGGCTTCGCGCCCAATAGCAGCAGTCCCTTCCCGCTTCAGTGACA	2999
QY	4686	AGCTCGAGCAGCTCGCGCAAGGAAGCCCGTTCGTCGCGAGCCACGATAGCGCGGTGCC	4745
Db	3000	AGCTCGAGCAGCTCGCGCAAGGAAGCCCGTTCGTCGCGAGCCACGATAGCGCGGTGCC	3059
QY	4746	TCGTCTTCAGTTCATTTCAGGCGCACCGGACAGTTCGCTTTCGACAAAAGAACCGGCGC	4805
Db	3060	TCGTCTTCAGTTCATTTCAGGCGCACCGGACAGTTCGCTTTCGACAAAAGAACCGGCGC	3119
QY	4806	CCCTCGCTGACAGCCGGAACAAGCGCGCATCAGAGCAGCCGATTCGTTGTGCCAG	4865
Db	3120	CCCTCGCTGACAGCCGGAACAAGCGCGCATCAGAGCAGCCGATTCGTTGTGCCAG	3179
QY	4866	TCATAGCCGAATAGCTCTCCACCCAGCGCGGAGAACCTGCTGCAATCCATCTTGT	4925
Db	3180	TCATAGCCGAATAGCTCTCCACCCAGCGCGGAGAACCTGCTGCAATCCATCTTGT	3239
QY	4926	TCAATCATGCGAAACGATCCTCATCTCTCTTTCATCAGATCTTGATCCCTCGGCCAT	4985

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Db	3240	TCATCATGCGAAGCGATCCTCATCTGTCTCTTTGATCAGATCTTGATCCCTCGCCAT	3299
Qy	4986	CAGATCCTTGGCGGCAAGAGCCATCCAGTTTACTTTGACGGGCTTCCCAACCTTACCA	5045
Db	3300	CAGATCCTTGGCGGCAAGAGCCATCCAGTTTACTTTGACGGGCTTCCCAACCTTACCA	3359
Qy	5046	GAGGGCGCCCGAGCTGGCAATTCCGTTGCTGTGTCATATAAACCGCCCGAGTCTAGC	5105
Db	3360	GAGGGCGCCCGAGCTGGCAATTCCGTTGCTGTGTCATATAAACCGCCCGAGTCTAGC	3419
Qy	5106	TATGCCCATGTAAGCCCACTGCAAGCTACCTGCTTCTCTT	5146
Db	3420	AACTGTTGGGAAGGGCGATCGGTGGGGCCCTCTCGCTATT	3460

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Job time : 1981 secs

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OM nucleic - nucleic search, using sw model

Run on: August 4, 2004, 04:18:10 ; Search time 333 Seconds  
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Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 682709 seqs, 277475446 residues

Total number of hits satisfying chosen parameters: 1365418

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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5: /cgn2\_6/ptodata/2/ina/PCTUS\_COMB.seq.\*  
6: /cgn2\_6/ptodata/2/ina/backfiles1.seq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	DB ID	Description
1	2240	42.4	8349	4	US-09-186-002-16
2	1793.4	33.9	4800	4	US-09-554-929-1
3	1652.4	31.3	5594	4	US-09-380-190A-29
4	1618.2	30.6	6561	4	US-09-380-190A-30
5	1602.2	30.3	5707	2	US-08-472-809B-8
6	1571.6	29.7	4665	3	US-08-948-378A-7
7	1571.6	29.7	4665	3	US-09-169-425C-7
8	1571.6	29.7	4665	4	US-09-759-960-7
9	1570	29.7	4518	4	US-09-380-190A-26
10	1570	29.7	4896	4	US-09-533-220A-4
11	1570	29.7	6139	2	US-08-751-767A-7
12	1569.8	29.7	4748	4	US-09-796-575-4
13	1569.8	29.7	4992	4	US-09-796-575-5
14	1569.8	29.7	8797	2	US-08-723-306-6
15	1569.8	29.7	8797	5	PCT-US96-10041-6
16	1569.8	29.7	11093	2	US-08-723-306-5
17	1569.8	29.7	11093	5	PCT-US96-10041-5
18	1564.2	29.6	5532	4	US-08-961-888-40
19	1501.4	28.4	6795	4	US-09-380-190A-22
20	1501.4	28.4	8574	4	US-09-554-572-3
21	1501.4	28.4	9093	4	US-09-380-190A-23
22	1501.4	28.4	9093	4	US-09-554-572-2
23	1501.4	28.4	9145	4	US-09-554-572-1
24	1501	28.4	9458	4	US-09-380-190A-20
25	1501	28.4	5754	4	US-09-380-190A-18
26	1501	28.4	5754	4	US-09-380-190A-19
27	1501	28.4	6225	4	US-09-380-190A-1

C	28	1501	28.4	6321	4	US-09-380-190A-17	Sequence 17, Appl
C	29	1501	28.4	6359	4	US-09-380-190A-15	Sequence 15, Appl
C	30	1501	28.4	6891	4	US-09-380-190A-16	Sequence 16, Appl
C	31	1501	28.4	8657	4	US-09-380-190A-14	Sequence 14, Appl
	32	1490.4	28.2	3974	3	US-09-026-343-33	Sequence 33, Appl
	33	1490.4	28.2	3974	3	US-09-042-105-16	Sequence 16, Appl
	34	1490.4	28.2	3974	3	US-09-044-856A-7	Sequence 7, Appl
	35	1490.4	28.2	3974	3	US-09-023-082A-147	Sequence 147, App
	36	1490.4	28.2	3974	3	US-09-044-855A-7	Sequence 7, Appl
	37	1490.4	28.2	3974	3	US-09-078-670-4	Sequence 4, Appl
	38	1490.4	28.2	3974	4	US-09-026-408-14	Sequence 14, Appl
	39	1490.4	28.2	3974	4	US-09-362-871-33	Sequence 33, Appl
	40	1490.4	28.2	3974	4	US-09-627-154-4	Sequence 4, Appl
	41	1490.4	28.2	3974	4	US-09-027-287-50	Sequence 50, Appl
	42	1490.4	28.2	3974	4	US-09-437-602-4	Sequence 4, Appl
	43	1490.4	28.2	3974	4	US-09-252-656B-50	Sequence 50, Appl
	44	1490.4	28.2	3974	4	US-09-248-998-147	Sequence 147, App
	45	1490.4	28.2	3974	4	US-09-105-470B-25	Sequence 25, Appl

ALIGNMENTS

RESULT 1  
US-09-186-002-16  
; Sequence 16, Application US/09186002B  
; Patent No. 6489542  
; GENERAL INFORMATION:  
; APPLICANT: Corbin, David R.  
; TITLE OF INVENTION: Improved Method for Transforming Plants to Express  
; TITLE OF INVENTION: delta-Endotoxins  
; FILE REFERENCE: 38-21(13547) US Pat No. 6489542 09/186,002  
; CURRENT APPLICATION NUMBER: US/09/186,002B  
; CURRENT FILING DATE: 1998-11-04  
; NUMBER OF SEQ ID NOS: 18  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 16  
; LENGTH: 8349  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; NAME/KEY: gene  
; LOCATION: (3666)..(5573)  
; OTHER INFORMATION: completely synthesized  
US-09-186-002-16

Query Match	42.4%	Score 2240;	DB 4;	Length 8349;
Best Local Similarity	93.4%	Pred. No. 0;		
Matches 2409;	Conservative	0;	Mismatches	25; Indels 144; Gaps 1;
QY	2706	CTAGAGCTAATCATGTCTAGCTAGTGTTCCTGTGTGAATTTGTTATCCGCTCAAAATTC	2765	
Db	5911	CTTGGCGTAATCATGTCTAGCTAGTGTTCCTGTGTGAATTTGTTATCCGCTCAAAATTC	5970	
QY	2766	ACACACATACACGCGGAGCATAAAGTGTAAAGCTCGGCTGCTTAATGAGTGAGCTA	2825	
Db	5971	ACACACATACACGCGGAGCATAAAGTGTAAAGCTCGGCTGCTTAATGAGTGAGCTA	6030	
QY	2826	ACTCATTAAATGCGTTCGCTCTACTGCCCTTCCAGTCCGGAACCTGTCTGCGCA	2885	
Db	6031	ACTCATTAAATGCGTTCGCTCTACTGCCCTTCCAGTCCGGAACCTGTCTGCGCA	6090	
QY	2886	GCTGATTAAATGCGTTCGCGCAACGCGGAGAGCGGTTTTCGCTATTTGGCGCTCTTC	2945	
Db	6091	GCTGATTAAATGCGTTCGCGCAACGCGGAGAGCGGTTTTCGCTATTTGGCGCTCTTC	6150	
QY	2946	CGCTTCCTCGCTCATGCTGCTCGCTCGCTCGCTCGCTCGCTCGCTCGCTCGCT	3005	
Db	6151	CGCTTCCTCGCTCATGCTGCTCGCTCGCTCGCTCGCTCGCTCGCTCGCTCGCT	6210	
QY	3006	TCACCTCAAGCGCGTAAATACGTTATCCACAGATCAGGGATACGCGGAAGAAAT	3065	



Db	6211	TCACTCAAAGCGGTAATAACGGTTATCCACAGAAATCAGGGGATTAACGACGAAAGAACAT	6270	QY	4146	AACTCGTCAAGAAAGCGGATAGAACCGGATCGCTGCGAAATCGGGAGCGGCGATACCGGTAA	4205
QY	3066	GTGAGCAAAAGCGGACAGAAAGCGGACAGAAACCGTAAAGGCGCGGTTGCTGGCGTTTTT	3125	Db	7207	AACTCGTCAAGAAAGCGGATAGAACCGGATCGCTGCGAAATCGGGAGCGGCGATACCGGTAA	7266
Db	6271	GTGAGCAAAAGCGGACAGAAAGCGGACAGAAACCGTAAAGGCGCGGTTGCTGGCGTTTTT	6330	QY	4206	AGCACGAGAAAGCGGTACGCCCATTCGCGCGCAAGCTCTTCAGCAATATCACGGGTAGCC	4265
QY	3126	CCATAGGCTCGGCCCGCTGACGAGCATCAAAAATCGAGCTCAAGTCAGAGGTGGCG	3185	Db	7267	AGCACGAGAAAGCGGTACGCCCATTCGCGCGCAAGCTCTTCAGCAATATCACGGGTAGCC	7326
Db	6331	CCATAGGCTCGGCCCGCTGACGAGCATCAAAAATCGAGCTCAAGTCAGAGGTGGCG	6390	QY	4266	AACGCTATGTCTCTGATAGGGTTCGCGCACACCCAGCGCGCCACAGTTCGATGAATCCAGAA	4325
QY	3186	AAACCCGACAGGACTATAAAGATACAGGCGTTTTCCCGTGGAACTCCCTCGTGGCTC	3245	Db	7327	AACGCTATGTCTCTGATAGCGTTCGCGCACACCCAGCGCGCCACAGTTCGATGAATCCAGAA	7386
Db	6391	AAACCCGACAGGACTATAAAGATACAGGCGTTTTCCCGTGGAACTCCCTCGTGGCTC	6450	QY	4326	AAGCGGCCATTTTCCACCATGATATTCGCAAGCAGGATCGCCATGGGTCAACAGCAGAA	4385
QY	3246	TCCTGTTCCGACCTCGCGCTTACCGGATACCTGTCGCGCTTTTCCTCTCGGAAGCGT	3305	Db	7387	AAGCGGCCATTTTCCACCATGATATTCGCAAGCAGGATCGCCATGGGTCAACAGCAGAA	7446
Db	6451	TCCTGTTCCGACCTCGCGCTTACCGGATACCTGTCGCGCTTTTCCTCTCGGAAGCGT	6510	QY	4386	TCCTCGCGCTCGGGCATCGCGCTTGAGCCTTGGCGAAACAGTTTCGCTGGCGGAGCCCC	4445
QY	3306	GGCGCTTCTCATAGCTCAAGCTGAGGTATCTCAGTTTCGGTGTAGGTGCTTCGCTCAA	3365	Db	7447	TCCTCGCGCTCGGGCATCGCGCTTGAGCCTTGGCGAAACAGTTTCGCTGGCGGAGCCCC	7506
Db	6511	GGCGCTTCTCATAGCTCAAGCTGAGGTATCTCAGTTTCGGTGTAGGTGCTTCGCTCAA	6570	QY	4446	TGATGCTCTTCGTCAGATCATCTCTGATCGAACAAGACCGGCTTCCATCCGAGTACGTGCT	4505
QY	3366	GCTGGGCTGTGTGACGAACCCCGGTTGAGCCGACCGCTTCGCGCTTATCCGCTAACTA	3425	Db	7507	TGATGCTCTTCGTCAGATCATCTCTGATCGAACAAGACCGGCTTCCATCCGAGTACGTGCT	7566
Db	6571	GCTGGGCTGTGTGACGAACCCCGGTTGAGCCGACCGCTTCGCGCTTATCCGCTAACTA	6630	QY	4506	CGCTCGATGCGATGTTTTCGCTTGGTGGTGAATGGGAGGTAGCCGATCAAGCGTATGC	4565
QY	3426	TCGTCCTTGAAGTCCAAACCCGCTGAGACAGCTTATCGCCACTGGCAGCAGCCACTGGTAA	3485	Db	7567	CGCTCGATGCGATGTTTTCGCTTGGTGGTGAATGGGAGGTAGCCGATCAAGCGTATGC	7626
Db	6631	TCGTCCTTGAAGTCCAAACCCGCTGAGACAGCTTATCGCCACTGGCAGCAGCCACTGGTAA	6690	QY	4566	AGCGCGCGCATTCGATCAGCCATGATGATCTTCCTCGGCAAGGAGCAAGGTGAGATGAC	4625
QY	3486	CAGGATTCAGAGCAGGAGTATGAGCGGTGCTACAGAGTTCCTGAAGTGGTGGCTTAA	3545	Db	7627	AGCGCGCGCATTCGATCAGCCATGATGATCTTCCTCGGCAAGGAGCAAGGTGAGATGAC	7686
Db	6691	CAGGATTCAGAGCAGGAGTATGAGCGGTGCTACAGAGTTCCTGAAGTGGTGGCTTAA	6750	QY	4626	AGGAGATCTTCGCGCGCATCTTCGCGCAATAGCAGCCAGTCCCTTCGCGCTTCAAGTAC	4685
QY	3546	CTACGGCTACACTAGAGAACAGTATTTGGTATCTGCGCTCTGCTGAGCCAGTACCTT	3605	Db	7687	AGGAGATCTTCGCGCGCATCTTCGCGCAATAGCAGCCAGTCCCTTCGCGCTTCAAGTAC	7746
Db	6751	CTACGGCTACACTAGAGAACAGTATTTGGTATCTGCGCTCTGCTGAGCCAGTACCTT	6810	QY	4686	ACGTCGAGCACAGCTGGCGAAGGAAACGCGCGTCTGTCGAGCACAGTACCGCGCTGCC	4745
QY	3606	CGGAAAGAGTGTGAGTCTTGATCCGGCAACCAACACCGCTGGTAGCGGTGTTT	3665	Db	7747	ACGTCGAGCACAGCTGGCGAAGGAAACGCGCGTCTGTCGAGCACAGTACCGCGCTGCC	7806
Db	6811	CGGAAAGAGTGTGAGTCTTGATCCGGCAACCAACACCGCTGGTAGCGGTGTTT	6870	QY	4746	TCGTCCTGCAAGTTCATTCAGGCGACCGGACAGCTCGGTCTTGACAAAAGAACCGGCGCG	4805
QY	3666	TTTTGTTTCAAGCAGCAGATTCAGCGCAGAAAAAAGATCTCAAGAGATCCTTTGAT	3725	Db	7807	TCGTCCTGCAAGTTCATTCAGGCGACCGGACAGCTCGGTCTTGACAAAAGAACCGGCGCG	7866
Db	6871	TTTTGTTTCAAGCAGCAGATTCAGCGCAGAAAAAAGATCTCAAGAGATCCTTTGAT	6930	QY	4806	CCCTGCGCTCACAGCCGGAACAGCGGCGCATCAGAGCAGCGGATGCTGTTGTGCGCCAG	4865
QY	3726	CTTTTCTACGGGCTGACGCTCAGTGAAGCAAACTCAGTTTAAAGGATTTTGTTCAT	3785	Db	7867	CCCTGCGCTCACAGCCGGAACAGCGGCGCATCAGAGCAGCGGATGCTGTTGTGCGCCAG	7926
Db	6931	CTTTTCTACGGGCTGACGCTCAGTGAAGCAAACTCAGTTTAAAGGATTTTGTTCAT	6990	QY	4866	TCATAGCCGAAATAGCTCTCCACCCAGCGCGCGGAGAACCTGGGTGCATATCCATCTTGT	4925
QY	3786	GAGATTATCGTCGACCAAGCGGCGATCGTGCCTCCCACTCTCTGAGTTTCGGGGCATG	3845	Db	7927	TCATAGCCGAAATAGCTCTCCACCCAGCGCGCGGAGAACCTGGGTGCATATCCATCTTGT	7986
Db	6991	GAGATTATCAAAAGGATCTTCACTAGATCCTT	7024	QY	4926	TCAATCATGCGAAAGGATCTTCATCTTGTCTCTTGATCAGATCTTGATCCCTCGCGCAT	4985
QY	3846	GATGCGCGGATAGCCGCTGCTGTTTCTCGGATCGCGAGCGGATTTGCACTCCCGGTAGAA	3905	Db	7987	TCAATCATGCGAAAGGATCTTCATCTTGTCTCTTGATCAGATCTTGATCCCTCGCGCAT	8046
Db	7025	-----	7024	QY	4986	CAGATCTTTCGCGGCAAGAAAGCCATCCAGTTTACTTTGAGGGCTTCCCAACTTACCA	5045
QY	3906	CTCCGCGAGTCTGTCAGCTCAGGACAGCTGAACCAACTCGCGAGGGATCGAGCCC	3965	Db	8047	CAGATCTTTCGCGGCAAGAAAGCCATCCAGTTTACTTTGAGGGCTTCCCAACTTACCA	8106
Db	7025	-----	7026	QY	5046	GAGGCGCGCCAGCTGGCAATTCGCTTGGTTCGCTTCTTCTTTCGCGCTTTCGCTTTCGCTT	5105
QY	3966	GGGGTGGCGAAGAACTCCAGCATGAGATPCCCGGCTGGAGGATCATCCAGCGGGCTC	4025	Db	8107	GAGGCGCGCCAGCTGGCAATTCGCTTGGTTCGCTTCTTCTTTCGCGCTTTCGCTTTCGCTT	8166
Db	7027	GGGGTGGCGAAGAACTCCAGCATGAGATPCCCGGCTGGAGGATCATCCAGCGGGCTC	7086	QY	5106	TATCGCCATGTAAGCCCACTGCAAGTACCTGCTTCTTCTTTCGCGCTTTCGCTTTCGCTT	5165
QY	4026	CCGGAACAGATTCCGAGCCCAACCTTTCATAGAGCGGGGTGGAAATCGAAATCTCG	4085	Db	8167	TATCGCCATGTAAGCCCACTGCAAGTACCTGCTTCTTCTTTCGCGCTTTCGCTTTCGCTT	8226
Db	7087	CCGGAACAGATTCCGAGCCCAACCTTTCATAGAGCGGGGTGGAAATCGAAATCTCG	7146	QY	5166	GTCCAGATAGCCAGTGTGATTCATTCGCGGCTGACGACCGGTTCTGCGGAGTGGCT	5225
QY	4086	TGATGCGAGTTGGGCTGCTTGGTTCATTTTCGAGTTCGAGTTCGAGTTCGAGTTCGAGT	4145	Db	8227	GTCCAGATAGCCAGTGTGATTCATTCGCGGCTGACGACCGGTTCTGCGGAGTGGCT	8286
Db	7147	TGATGCGAGTTGGGCTGCTTGGTTCATTTTCGAGTTCGAGTTCGAGTTCGAGTTCGAGT	7206				

Qy	5226	TTCTACGTGTTCCGCTTCCTTTAGCAGCCCTTGCGCCCTGAGTGTGCGGAGCGTG	5283
Db	8287	TTCTACGTGTTCCGCTTCCTTTAGCAGCCCTTGCGCCCTGAGTGTGCGGAGCGTG	8344

4967 CATAGCCGAATAGCTCTTCCACCAAGCGCGGAGAACTCTGGTGGAAATCCATCTTGT 4926  
 3236 CATAGCCGAATAGCTCTTCCACCAAGCGCGGAGAACTCTGGTGGAAATCCATCTTGT 3177  
 4927 CAATCATCGGAAACGATCTCTATCTCTCTTGTATCAGATCTTATCCCTTGGCCATC 4986  
 3176 CAATCATCGGAAACGATCTCTATCTCTCTTGTATCAGATCTTATCCCTTGGCCATC 3117  
 4987 AGATCTTGGCGGGAAGAAAGCAATCCAGTTTACCTTTCAGGGCTTCCAACTTACCAG 5046  
 3116 AGATCTTGGCGGGAAGAAAGCAATCCAGTTTACCTTTCAGGGCTTCCAACTTACCAG 3057  
 5047 AGGCGCGCCCACTCGGCAATCCGGTTCGCTTGTCTGATCAAAACCGCCAGTCTAGCT 5106  
 3056 AGGCGCGCCCACTCGGCAATCCGGTTCGCTTGTCTGATCAAAACCGCCAGTCTAGCT 2997  
 5107 ATCGCATGTAGCCCACTGCAAGCTTCTCTCTCTTTCGCTTGGCTTGGCTTTCCTTGT 5166  
 2996 ATCGCATGTAGCCCACTGCAAGCTTCTCTCTCTTTCGCTTGGCTTGGCTTTCCTTGT 2937  
 5167 TCCAGATAGCCCACTGCAAGCTTCTCTCTCTTTCGCTTGGCTTGGCTTTCCTTGT 5226  
 2936 TCCAGATAGCCCACTGCAAGCTTCTCTCTCTTTCGCTTGGCTTGGCTTTCCTTGT 2877  
 5227 TCTAGCTGTTCGCTTTCCTTTCAGAGCCCTTGGCCCTGAGTCTTGGCGGAGCGGTG 5283  
 2876 TCTAGCTGTTCGCTTTCCTTTCAGAGCCCTTGGCCCTGAGTCTTGGCGGAGCGGTG 2820

RESULT 3

US-09-380-190A-29/c  
 : Sequence 29, Application US/09380190A  
 : Patent No. 6410220

GENERAL INFORMATION:

APPLICANT: NATURE TECHNOLOGY CORPORATION, ET AL.  
 TITLE OF INVENTION: SELF-ASSEMBLING GENES, VECTORS AND USES THEREOF

NUMBER OF SEQUENCES: 74

CORRESPONDENCE ADDRESS:

ADDRESSEE: MUEITING, RAASCH & GEBHARDT, P.A.

STREET: 119 NORTH FOURTH STREET, SUITE 203

CITY: MINNEAPOLIS

STATE: MINNESOTA

COUNTRY: USA

ZIP: 55401

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent In Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/380.190A

FILING DATE: 26-Aug-1999

CLASSIFICATION: <unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: PCT/US98/03918

FILING DATE: 28-FEB-98

ATTORNEY/AGENT INFORMATION:

NAME: MUEITING, ANN M.

REGISTRATION NUMBER: 33,977

REFERENCE/DOCKET NUMBER: 228.00010201

TELECOMMUNICATION INFORMATION:

TELEPHONE: 612-305-1217

TELEFAX: 612-305-1228

INFORMATION FOR SEQ ID NO: 29:

SEQUENCE CHARACTERISTICS:

LENGTH: 5594 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: DNA (genomic)

SEQUENCE DESCRIPTION: SEQ ID NO: 29:

US-09-380-190A-29

Query Match 31.3%; Score 1652.4; DB 4; Length 5594;  
 Best Local Similarity 85.4%; Pred. No. 0;  
 Matches 1916; Conservative 0; Mismatches 261; Indels 67; Gaps 4;

QY 3107 CCGGTTGCTGCGCTTTTCCATAGGCTCCGCCCCCTGACGAGCATCACAAAATCCAC 3166  
 DB 5591 CGGCGTCTGCGCTTTTCCATAGGCTCCGCCCCCTGACGAGCATCACAAAATCCAC 5532  
 QY 3167 GCTCAAGTCAGAGTGGCGAAACCGCAGAGCTATAAAGATACCAGGCGTTTCCCGCTG 3226  
 DB 5531 GCTCAAGTCAGAGTGGCGAAACCGCAGAGCTATAAAGATACCAGGCGTTTCCCGCTG 5472  
 QY 3227 GAAGCTCCCTCGTGGCTCTCTCTGTTCCGACCCCTCCGCTTACCGGATACCTGCGCT 3286  
 DB 5471 GAAGCTCCCTCGTGGCTCTCTCTGTTCCGACCCCTCCGCTTACCGGATACCTGCGCT 5412  
 QY 3287 TTCTCCCTTCGGAAGCGTGGCGCTTTCTCATAGCTCAGCTGATAGTATCTCAGTTCCG 3346  
 DB 5411 TTCTCCCTTCGGAAGCGTGGCGCTTTCTCAATGCTCAGCTGATAGTATCTCAGTTCCG 5352  
 QY 3347 TGTAGTCTGCTCCAGCTGGCTGTGTGCAAGACCCCGCTTCAAGCCGACCGCT 3406  
 DB 5351 TGTAGTCTGCTCCAGCTGGCTGTGTGCAAGACCCCGCTTCAAGCCGACCGCT 5292  
 QY 3407 GCGCTTATCCGTTAACTATCTGTTAGTCCAAACCGGTAAGACACGACTTATCCGAC 3466  
 DB 5291 GCGCTTATCCGTTAACTATCTGTTAGTCCAAACCGGTAAGACACGACTTATCCGAC 5232  
 QY 3467 TGGCAGCAGCACTGGTAAACAGATTAGCAGGAGGATGTAGCGGTGTCTACAGAGT 3526  
 DB 5231 TGGCAGCAGCACTGGTAAACAGATTAGCAGGAGGATGTAGCGGTGTCTACAGAGT 5172  
 QY 3527 TCTTGAAGTGTGGCTTAACCTACGCTACACTAGAAGAAACAGTATTTGGTATCTGCGCTC 3586  
 DB 5171 TCTTGAAGTGTGGCTTAACCTACGCTACACTAGAAGAAACAGTATTTGGTATCTGCGCTC 5112  
 QY 3587 TGCTGAAGCAGTTACCTTCGGAAGAAAGATTGGTAGCTCTTGTATCCGGAACAAACCA 3646  
 DB 5111 TGCTGAAGCAGTTACCTTCGGAAGAAAGATTGGTAGCTCTTGTATCCGGAACAAACCA 5052  
 QY 3647 CCGCTGGTAGCGGTGGTTTTTTTGTGCAAGCAGAGATTACGCGCAGAAAAGAGAT 3706  
 DB 5051 CCGCTGGTAGCGGTGGTTTTTTTGTGCAAGCAGAGATTACGCGCAGAAAAGAGAT 4992  
 QY 3707 CTCAGAGATCTTTTGTATCTTCTACGGGTCTGACGCTC-----AGTGGAAAG 3757  
 DB 4991 GGTGTGGGTCTTTTATTTAGCTCGGGAGCAGACGCGGCAACAGAGCAGAGAGCG 4932  
 QY 3758 AAAAATCACGTTAAGGATTTTGGTCAAGATTAATCGTCAACAAAGCGGCTCGTGC 3817  
 DB 4931 AACTGATTGGTTAGTTCAATTAAGGCACAGGTCATTTCAGGTCCTTGGGGCACCGTGA 4872  
 QY 3818 CTC-----CCCACTCCTGAGTTCGGGGCATGATGCGCGGATAGCCGCTG 3864  
 DB 4871 AACATCTGATGTTCTCTAGAACTGCTGAGGCTGGACCCATCTGGGGACCATCTGTT 4812  
 QY 3865 CTGGTTTCTGATGCGGACCGGATTTCG-----ACTGCGGTAGAACTCGCGGAG 3914  
 DB 4811 CTGGGCTGAGCGGGGCGGAGGAACTGCTTACACAGATATCTCTGTTTGGCCCATATCA 4752  
 QY 3915 GTCGTCAGGCTCAGGAGCAGCTGAACAACTCGGAGGGGATCGAGCCGGGGTGGGC 3974  
 DB 4751 GCTGTTCATCTGTTCTTGGCCCTGAGCGGGGAGGAACTGCTTACACAGATATCTCTG 4692  
 QY 3975 GAAGAACTCCAGCATGATATCCCGCTGGAGGATCATCCAGCGGCGGTCCCGGAAAC 4034  
 DB 4691 TTTGGCCCATATTCAGCTGTTCCATCTCTCTGACCTTGTATCTGAACTTCTTATTCTC 4632  
 QY 4035 GATTCCGGAAGCCCAACCTTTTCATAGAAGCGCGGTGGAATCGAAATCTCG----- 4085  
 DB 4631 AGTTATGATATTTTCCATGCTTGCATAATGCGGTTTAAAGCTAGCTTGCACAACTCA 4572

4086 -----TGATGCAGGTTGGGCGTTCGCTTGTTCGGTCATT 4119  
Db CAGGTGGGTCCTTTCAATCCCGCCCTTTTCTGGAGGTTGGGCGTCGCTTGTTCGGTCATT 4512  
4120 TCGAACCCAGAGTCCCGCTCAGAAAGAACTCGTCAAGAGGCGATAGAGGCGATGCGCT 4179  
Db TCGAACCCAGAGTCCCGCTCAGAAAGAACTCGTCAAGAGGCGATAGAGGCGATGCGCT 4452  
4180 CGGAATCGGAGCGCGGATACGTAAGACAGAGAAAGCGGTCAGCCATTGCGCGCAA 4239  
Db CGGAATCGGAGCGCGGATACGTAAGACAGAGAAAGCGGTCAGCCATTGCGCGCAA 4392  
4240 GCTCTTCAGCAATATCAGCGGTAGCAACGCTATGCTCTGATAGCGGTCGCGCACACCA 4299  
Db GCTCTTCAGCAATATCAGCGGTAGCAACGCTATGCTCTGATAGCGGTCGCGCACACCA 4332  
4300 GCGGCGCAGTCGATGAATCCAGAAAGCGGCCATTTCACCATGATATTCGCGAAGC 4359  
Db GCGGCGCAGTCGATGAATCCAGAAAGCGGCCATTTCACCATGATATTCGCGAAGC 4272  
4360 AGGCATCGCCATGGGTCACGACGAGATCTCGCGTGGGCGATGCGCGCTTGAGCCTGG 4419  
Db AGGCATCGCCATGGGTCACGACGAGATCTCGCGTGGGCGATGCGCGCTTGAGCCTGG 4212  
4420 CGAACAGTTCGGCTGGGCGGAGCCCTGATGCTCTTCGTCAGATCATCTGATCGACAA 4479  
Db CGAACAGTTCGGCTGGGCGGAGCCCTGATGCTCTTCGTCAGATCATCTGATCGACAA 4152  
4480 GACCGGTTTCATCCGAGTAGTGCTCGCTCGATGCGATGTTTCGCTTGGTGGTCGAATG 4539  
Db GACCGGTTTCATCCGAGTAGTGCTCGCTCGATGCGATGTTTCGCTTGGTGGTCGAATG 4092  
4540 GCGAGTAGCGGATCAAGCGTATGACGCGCGCATTCGATGATGATGATGATGATGATGAT 4599  
Db GCGAGTAGCGGATCAAGCGTATGACGCGCGCATTCGATGATGATGATGATGATGATGAT 4032  
4600 TCTCGCAGGAGCAAGTGATGATGACAGGAGATCTCTCCCGCGCATTCGCGCGCAATAGCA 4659  
Db TCTCGCAGGAGCAAGTGATGATGACAGGAGATCTCTCCCGCGCATTCGCGCGCAATAGCA 3972  
4660 GCGAGTCCCTTCGCTTCAAGTGAACGTCGAGCAGCTGCGGCAAGCAACGCCGCTCG 4719  
Db GCGAGTCCCTTCGCTTCAAGTGAACGTCGAGCAGCTGCGGCAAGCAACGCCGCTCG 3912  
4720 TGCCAGCAGCAGATAGCGGCTCGCTCGTTCGAGTTCATTCAGGCGACCGGACAGGT 4779  
Db TGCCAGCAGCAGATAGCGGCTCGCTCGTTCGAGTTCATTCAGGCGACCGGACAGGT 3852  
4780 CGGTCTTGACAAAGAACCGGGCGCCCTCGCTGACAGCGGCAACACGCGGCGATCAG 4839  
Db CGGTCTTGACAAAGAACCGGGCGCCCTCGCTGACAGCGGCAACACGCGGCGATCAG 3792  
4840 AGCAGCGATTGCTGTTGCGCAGTATAGCCGAATAGCCTCTCCACCAAGCGGCGC 4899  
Db AGCAGCGATTGCTGTTGCGCAGTATAGCCGAATAGCCTCTCCACCAAGCGGCGC 3732  
4900 GAGAACCTCGCTGCAATCATCTGTTCAATCATGCGAAACCATCTCATCTGCTCTTT 4959  
Db GAGAACCTCGCTGCAATCATCTGTTCAATCATGCGAAACCATCTCATCTGCTCTTT 3672  
4960 GATCAGATCTTGATCCCTTCGCCCATCAGATCCTTGGCGGCAAGAACCATCCAGTTTA 5019  
Db GATCAGATCTTGATCCCTTCGCCCATCAGATCCTTGGCGGCAAGAACCATCCAGTTTA 3612  
5020 CTTTCAGGGCTTCCCACTTACAGAGGCGCCCTCAGCTGGCAATTCGCTTGGCTTG 5079  
Db CTTTCAGGGCTTCCCACTTACAGAGGCGCCCTCAGCTGGCAATTCGCTTGGCTTG 3552  
5080 CTGTCCATAAAGCCCGAGTCTAGCTATCGCCATGTAAGCCCATGCAAGCTACTGCT 5139  
Db CTGTCCATAAAGCCCGAGTCTAGCTATCGCCATGTAAGCCCATGCAAGCTACTGCT 3492  
5140 TTCTCTTTCGCGTTCGCTTTCCCTTGTCCAGATAGCCAGTAGCTGATTCATCCGGG 5199

Db 3491 TTCTCTTTGGCGTTTCGCTTTCCCTTTGCCATAGCCAGTAGCTGATTCATCCGGG 3432  
QY 5200 GTACACACGTTTCGCGGACTGGCTTCTACGTTTCGCTTTCGCTTTAGCAGCCCTTGC 5259  
Db 3431 GTACACACGTTTCGCGGACTGGCTTCTACGTTTCGCTTTCGCTTTAGCAGCCCTTGC 3372  
QY 5260 GCCCTGAGTGTTCGCGGACGCGTG 5283  
Db 3371 GCCCTGAGTGTTCGCGGACGCGTG 3348  
RESULT 4  
US-09-380-190A-30/c  
; Sequence 30, Application US/09380190A  
; Patent No. 6410220  
; GENERAL INFORMATION:  
; APPLICANT: NATURE TECHNOLOGY CORPORATION, ET AL.  
; TITLE OF INVENTION: SELF-ASSEMBLING GENES, VECTORS AND USES THEREOF  
; NUMBER OF SEQUENCES: 74  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: MUEITING, RAASCH & GEBHARDT, P.A.  
; STREET: 119 NORTH FOURTH STREET, SUITE 203  
; CITY: MINNEAPOLIS  
; STATE: MINNESOTA  
; COUNTRY: USA  
; ZIP: 55401  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent in Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/380,190A  
; FILING DATE: 26-Aug-1999  
; CLASSIFICATION: <Unknown>  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: PCT/US98/03918  
; FILING DATE: 28-FEB-98  
; ATTORNEY/AGENT INFORMATION:  
; NAME: MUEITING, ANN M.  
; REGISTRATION NUMBER: 33,977  
; REFERENCE/DOCKET NUMBER: 228.00010201  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 612-305-1217  
; TELEFAX: 612-305-1228  
; INFORMATION FOR SEQ ID NO: 30:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 6561 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: DNA (genomic)  
; SEQUENCE DESCRIPTION: SEQ ID NO: 30:  
US-09-380-190A-30

Query Match 30.6%; Score 1618.2; DB 4; Length 6561;  
Best Local Similarity 86.7%; Pred. No. 0;  
Matches 1911; Conservative 0; Mismatches 23; Indels 269; Gaps 1;  
QY 3081 GCAGAGCGCAGGAAACCGTAAAGGCGCGGTCGCTGGGTTTTCATAGGCTCGGCC 3140  
Db GCAGGTGTACTCGAGCGCGGCGATCTCGCGTGTCTGCGGTTTTCATAGGCTCGGCC 2246  
QY 3141 CCCTGACGAGCATCAAAAAATCGACGCTCAAGTCAGAGGTGGGAAACCCACAGGACT 3200  
Db CCCTGACGAGCATCAAAAAATCGACGCTCAAGTCAGAGGTGGGAAACCCACAGGACT 2186  
QY 3201 ATAAAGATACAGGGGTTTCCCTTGGAAAGCTCCCTCGTGGCTCTCTGTTTCGAGCCT 3260  
Db ATAAAGATACAGGGGTTTCCCTTGGAAAGCTCCCTCGTGGCTCTCTGTTTCGAGCCT 2126

Thu Aug 5 08:55:54 2004

QY	3261	GCCTTTACCGGATACCTGTCCTGCTTCTCCCTTCGGGAGCGTGGCGTTTCTCATAG	3320	Db	1314	ACCATGATATTGGCAAGCAGGACATCGCCATGCGGTACAGAGATCTTCGCCCTCGGC	1255
Db	2125	GCCTTTACCGGATACCTGTCCTGCTTCTCCCTTCGGGAGCGTGGCGTTTCTCATAG	2066	QY	4401	ATGCGCGCTTGGACCTGGCGAAGCAGTTCGGCTGGCGAGCCCTGATGCTCTTCGTC	4460
QY	3321	CTCAGCTGTAGGTATCTCAGTTTGGGTGGGTGGGTGGGTGGGTGGGTGGGTGGGT	3380	Db	1254	ATGCGCGCTTGGACCTGGCGAAGCAGTTCGGCTGGCGAGCCCTGATGCTCTTCGTC	1195
Db	2065	CTCAGCTGTAGGTATCTCAGTTTGGGTGGGTGGGTGGGTGGGTGGGTGGGTGGGT	2006	QY	4461	AGATCATCTGATCGAACAAGACCGCTTCCATCCGAGTACGCTGCTGCTGATGATGT	4520
QY	3381	CGAACCCCTGTTTACCGGAGCGCTGCTTATCCGCTTACCTGCTGCTGCTGCTGCT	3440	Db	1194	AGATCATCTGATCGAACAAGACCGCTTCCATCCGAGTACGCTGCTGCTGATGATGT	1135
Db	2005	CGAACCCCTGTTTACCGGAGCGCTGCTTATCCGCTTACCTGCTGCTGCTGCTGCT	1946	QY	4521	TTCCGCTTGGTGGTCCGAATGGGACAGTACCGGATCAAGCTATGAGCGCGCATGCA	4580
QY	3441	CCCGGTAAAGACACAGCTTATCCCACTGGCAGCAGCCACTGGTAACAGATAGCAGG	3500	Db	1134	TTCCGCTTGGTGGTCCGAATGGGACAGTACCGGATCAAGCTATGAGCGCGCATGCA	1075
Db	1945	CCCGGTAAAGACACAGCTTATCCCACTGGCAGCAGCCACTGGTAACAGATAGCAGG	1886	QY	4581	TCAGCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG	4640
QY	3501	GAGGTATGAGCGGTGCTACAGAGTCTTGAAGTGGTGGCTAACTACGCTACACTAG	3560	Db	1074	TCAGCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG	1015
Db	1885	GAGGTATGAGCGGTGCTACAGAGTCTTGAAGTGGTGGCTAACTACGCTACACTAG	1826	QY	4641	GGCACTTCGCCCAATAGCAGGACGCTCCCTTCCCGCTTCCAGTACAGTACAGTAC	4700
QY	3561	AAGACAGTATTTGGTATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	3620	Db	1014	GGCACTTCGCCCAATAGCAGGACGCTCCCTTCCCGCTTCCAGTACAGTACAGTAC	955
Db	1825	AAGACAGTATTTGGTATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	1766	QY	4701	GGCACTTCGCCCAATAGCAGGACGCTCCCTTCCCGCTTCCAGTACAGTACAGTAC	4760
QY	3621	TAGCTCTTGTATCCGGCAAAACAAACACCGCTGGTACGCGTGGTGGTGGTGGT	3680	Db	954	GGCACTTCGCCCAATAGCAGGACGCTCCCTTCCCGCTTCCAGTACAGTACAGTAC	895
Db	1765	TAGCTCTTGTATCCGGCAAAACAAACACCGCTGGTACGCGTGGTGGTGGTGGT	1706	QY	4761	TTTCAGGACACCGGACAGGTCGGTCTTGAACAAAGAAACCGGCGCGCTTCGCTG	4820
QY	3681	GCAGATACGCGCAGAAAGGATCTCAAGAGATCTTGAATCTTCTTACGCGGTC	3740	Db	894	TTTCAGGACACCGGACAGGTCGGTCTTGAACAAAGAAACCGGCGCGCTTCGCTG	835
Db	1705	GCAGATACGCGCAGAAAGGATCTCAAGAGATCTTGAATCTTCTTACGCGGTC	1696	QY	4821	CGGAAACACCGGCGCATCAGACAGCGGATTTGTCTGTGTGCGCGCATAGCGGAT	4880
QY	3741	TGAAGCTCAGTGGAAACGAAACTCAGCTTAAAGGATTTTGGTATGAGATTAAT	3800	Db	834	CGGAAACACCGGCGCATCAGACAGCGGATTTGTCTGTGTGCGCGCATAGCGGAT	775
Db	1695	TGAAGCTCAGTGGAAACGAAACTCAGCTTAAAGGATTTTGGTATGAGATTAAT	1696	QY	4881	CTTCTCACCCAAAGCGCGGAGAACTCGCTGCTGCTGCTGCTGCTGCTGCTGCTG	4940
QY	3801	CAAGCGGCTATGCTGCTCCCACTCCCTGCTGCTGCTGCTGCTGCTGCTGCTG	3860	Db	774	CTTCTCACCCAAAGCGCGGAGAACTCGCTGCTGCTGCTGCTGCTGCTGCTGCTG	715
Db	1695	CAAGCGGCTATGCTGCTCCCACTCCCTGCTGCTGCTGCTGCTGCTGCTGCTG	1696	QY	4941	GATCTCATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	5000
QY	3861	GCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	3920	Db	714	GATCTCATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	655
Db	1695	GCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	1696	QY	5001	AAGAAAGCATCCAGTTTACTTTGCGGCTTCCCAACCTTACAGAGGCGCGCCAG	5060
QY	3921	CAGCCTCAGCAGCAGTGAACCAACTCGCGAGGGATCAGCCCGGGTGGCGAAGAA	3980	Db	654	AAGAAAGCATCCAGTTTACTTTGCGGCTTCCCAACCTTACAGAGGCGCGCCAG	595
Db	1695	CAGCCTCAGCAGCAGTGAACCAACTCGCGAGGGATCAGCCCGGGTGGCGAAGAA	1675	QY	5061	GGCAATTCGGTTCGCTTGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	5120
QY	3981	CTCCAGCATGAGATCCCGGCTGGAGGATCATCCAGCGCGGCTCCCGGAAAGCATTC	4040	Db	594	GGCAATTCGGTTCGCTTGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	535
Db	1674	CTCCAGCATGAGATCCCGGCTGGAGGATCATCCAGCGCGGCTCCCGGAAAGCATTC	1615	QY	5121	CCACTGCAAGCTACCTGCTTCTTTCGCTTTCGCTTTCGCTTTCGCTTTCGCTT	5180
QY	4041	GAAGCCCACTTTTCATAGAGGCGGCTGGATCGAAATCTCGTATGCGAGTTGGG	4100	Db	534	CCACTGCAAGCTACCTGCTTCTTTCGCTTTCGCTTTCGCTTTCGCTTTCGCTT	475
Db	1614	GAAGCCCACTTTTCATAGAGGCGGCTGGATCGAAATCTCGTATGCGAGTTGGG	1555	QY	5181	TAGCTGCAATTCATTCGCGGCTGACACCGTTTTCGCGGATGCTGCTTTCGCTT	5240
QY	4101	CGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	4160	Db	474	TAGCTGCAATTCATTCGCGGCTGACACCGTTTTCGCGGATGCTGCTTTCGCTT	415
Db	1554	CGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	1495	QY	5241	TTCTTTTAGCAGCGCTTTCGCGGCTGAGTGTTCGCGGAGCGGTG	5283
QY	4161	CGATAGAGGCGATTCGCTGCGGATTCGGGAGCGCGATACCGTAAGCAGCAGGCG	4220	Db	414	TTCTTTTAGCAGCGCTTTCGCGGCTGAGTGTTCGCGGAGCGGTG	372
Db	1494	CGATAGAGGCGATTCGCTGCGGATTCGGGAGCGCGATACCGTAAGCAGCAGGCG	1435	QY			
QY	4221	TCAGCCCATTCGCGCGCAAGCTCTTCAGCAATATCAGCGGTAGCCAACTGCTGTA	4280	Db			
Db	1434	TCAGCCCATTCGCGCGCAAGCTCTTCAGCAATATCAGCGGTAGCCAACTGCTGTA	1375	QY			
QY	4281	TAGCGGTCCGACACACCGCGCGCAAGCTGCTGCTGCTGCTGCTGCTGCTGCTG	4340	Db			
Db	1374	TAGCGGTCCGACACACCGCGCGCAAGCTGCTGCTGCTGCTGCTGCTGCTGCTG	1315	QY			
QY	4341	ACCATGATATTGGCAAGCAGGATCGCCATCGGCTCAGCAGGATCTTCGCGCTGG	4400	Db			

RESULT 5  
 US-08-472-809B-8  
 ; Sequence 8, Application US/08472809B  
 ; Patent No. 5925564  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Schwartz, Robert J.  
 ; APPLICANT: DeMayo, Franco J.  
 ; APPLICANT: O'Malley, Bert W.  
 ; TITLE OF INVENTION: Expression Vector Systems and



4206 AGCAGGAGGAGGCTCAGCCCAATTCGCGCCAGCTCTTACGAAATATACCGGGTAGCC 4265  
4622 AGCAGGAGGAGGCTCAGCCCAATTCGCGCCAGCTCTTACGAAATATACCGGGTAGCC 4681  
4266 AACCTATGCTCTGATAGCGGTGCGCACACCCAGCGGCCACAGTGCATGAATCCAGAA 4325  
4682 AACGCTATGCTCTGATAGCGGTGCGCACACCCAGCGGCCACAGTGCATGAATCCAGAA 4741  
4326 AAGCGGCAATTTCCACCATGATATTGGCAAGCAGGCTCGCCATGGGTCAACGACGAGA 4385  
4742 AAGCGGCAATTTCCACCATGATATTGGCAAGCAGGCTCGCCATGGGTCAACGACGAGA 4801  
4386 TCCTCGCGCTCGGGCATCGCGGCTTGAGCCTGGCGAAACAGTTCGGCTGGCGCGAGCCCC 4445  
4802 TCCTCGCGCTCGGGCATCGCGGCTTGAGCCTGGCGAAACAGTTCGGCTGGCGCGAGCCCC 4861  
4446 TGATGCTCTTCTGATCAGATCATCTCTGATCGACAGACCGGCTTCCATCCGAGTACGTCT 4505  
4862 TGATGCTCTTCTGATCAGATCATCTCTGATCGACAGACCGGCTTCCATCCGAGTACGTCT 4921  
4506 CGCTCGATGCGATGTTTCGCTTGTGTCGATGGCGCAGGTAGCCGGATCAAGCGTATGC 4565  
4922 CGCTCGATGCGATGTTTCGCTTGTGTCGATGGCGCAGGTAGCCGGATCAAGCGTATGC 4981  
4566 AGCCGCGCATTTGCATCGCCATGATGATATCTTTCTGGCAGGAGCAAGGTGATGAC 4625  
4982 AGCCGCGCATTTGCATCGCCATGATGATATCTTTCTGGCAGGAGCAAGGTGATGAC 5041  
4626 AGGAGATCTGCTCCCGGCACTTCGCGCAATAGCAGCGAGTCCCTTCCGCTTCAGTGACA 4685  
5042 AGGAGATCTGCTCCCGGCACTTCGCGCAATAGCAGCGAGTCCCTTCCGCTTCAGTGACA 5101  
4686 AGTTCAGCAGCAGCTCGCGAAGAACGCCGCTGTCGGCAGCAGCAGATAGCCGCGTGCC 4745  
5102 AGTTCAGCAGCAGCTCGCGAAGAACGCCGCTGTCGGCAGCAGCAGATAGCCGCGTGCC 5161  
4746 TCGTCTCTGCAATTCATTCAGGGCAGCCGACAGGTGCTTTGACAAAAGAACCGGGCGC 4805  
5162 TCGTCTCTGCAATTCATTCAGGGCAGCCGACAGGTGCTTTGACAAAAGAACCGGGCGC 5221  
4806 CCTTGGCTGACAGCGGAAACAGCGGCGCATCAGACAGCGGATGCTGCTTGTGCGCCAG 4865  
5222 CCTTGGCTGACAGCGGAAACAGCGGCGCATCAGACAGCGGATGCTGCTTGTGCGCCAG 5281  
4866 TCATAGCGGAATAGCCTCTCCACCCAGCGCGCGAGAACCTCGTGCAATCCATCTGT 4925  
5282 TCATAGCGGAATAGCCTCTCCACCCAGCGCGCGAGAACCTCGTGCAATCCATCTGT 5341  
4926 TCAATCATGCGAAACGATCTCTATCTCTGATCAGATCTTGTATCCCTCGCGCAT 4985  
5342 TCAATCATGCGAAACGATCTCTATCTCTGATCAGATCTTGTATCCCTCGCGCAT 5401  
4986 CAGATCTTGGCGGCAAGAACCATCAGTTACTTTTGAGGGCTTCCCAACCTTACCA 5045  
5402 CAGATCTTGGCGGCAAGAACCATCAGTTACTTTTGAGGGCTTCCCAACCTTACCA 5461  
5046 GAGGCGCCCGCAGCTGCGCAATTCGCGTTCGCTGCTGCTATATAAAGCCGCGCATGAC 5105  
5462 GAGGCGCCCGCAGCTGCGCAATTCGCGTTCGCTGCTGCTATATAAAGCCGCGCATGAC 5521  
5106 TATCGCCATGTAAGCCCATGTCAGAGCTACCTGCTTCTCTT 5146  
5522 AACTGTTGGGAAGGCGCATCGGTGCGGCGCTCTTGCTATT 5562

RESULT 6  
US-08-948-378A-7/c  
; Sequence 7, Application US/08948378A  
; Patent No. 6013258  
; GENERAL INFORMATION:  
; APPLICANT: Urban, Robert G.  
; APPLICANT: Chicz, Roman M.  
; APPLICANT: Collins, Edward J.

APPLICANT: Hedley, Mary Lynn  
TITLE OF INVENTION: IMMUNOGENIC PEPTIDES FROM  
THE HPV E7 PROTEIN  
NUMBER OF SEQUENCES: 19  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Fish & Richardson, P.C.  
STREET: 225 Franklin Street  
CITY: Boston  
STATE: MA  
COUNTRY: US  
ZIP: 02110-2804  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: Windows95  
SOFTWARE: FastSeq for Windows Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/948,378A  
FILING DATE: 09-OCT-1997  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER:  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Fraser, Janis K.  
REGISTRATION NUMBER: 34,819  
REFERENCE/DOCKET NUMBER: 08191/004001  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 617-542-5070  
TELEFAX: 617-543-8906  
TELEX: 200154  
INFORMATION FOR SEQ ID NO: 7:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 4665 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: circular  
MOLECULE TYPE: pBIOTOPHEPV  
US-08-948-378A-7

Query Match 29.7%; Score 1571.6; DB 3; Length 4665;  
Best Local Similarity 86.3%; Pred. No. 0;  
Matches 1850; Conservative 0; Mismatches 114; Indels 180; Gaps 3;  
Qy 3008 ACTCAAAGGCGGTAAATACGGTTATCCACAGAAATCAGGGGATACAGCAGGAAAGACATGT 3067  
Db 2624 AATGCATGGCGGTAAATACGGTTATCCACAGAAATCAGGGGATACAGCAGGAAAGACATGT 2565  
Qy 3068 GAGCAAAAGGCCAGCAAAAGGCCAGCAAAAGGCCAGCAAAAGGCCAGCAAAAGGCCAGCA 3127  
Db 2564 GAGCAAAAGGCCAGCAAAAGGCCAGCAAAAGGCCAGCAAAAGGCCAGCAAAAGGCCAGCA 2505  
Qy 3128 ATAGGCTCCGCGCCCTTCAGCAGCATCACAATAATCAGCCTCAAGTCAGAGGTGGCGAA 3187  
Db 2504 ATAGGCTCCGCGCCCTTCAGCAGCATCACAATAATCAGCCTCAAGTCAGAGGTGGCGAA 2445  
Qy 3188 ACCCGACAGACATATAAGATACAGCGGTTTCCCTTGGAGGCTCCCTCGTGGCTCTC 3247  
Db 2444 ACCCGACAGACATATAAGATACAGCGGTTTCCCTTGGAGGCTCCCTCGTGGCTCTC 2385  
Qy 3248 CTGTTCCGACCTTCGCGCTTACCGGATACCTGTCCGCTTCTCCCTTCGGGAAGCGTGG 3307  
Db 2384 CTGTTCCGACCTTCGCGCTTACCGGATACCTGTCCGCTTCTCCCTTCGGGAAGCGTGG 2325  
Qy 3308 GCTTTTCTCATAGCTCAGCGCTGATAGTATCTCAGTTCGGTGTAGTTCGTTCCGTTCCAGC 3367  
Db 2324 GCTTTTCTCATAGCTCAGCGCTGATAGTATCTCAGTTCGGTGTAGTTCGTTCCGTTCCAGC 2265  
Qy 3368 TGGGCTGTGTGCAAGAACCCCGGTTAGCCCGACCGCTCGCCTTATCCGTTACTATC 3427  
Db 2264 TGGGCTGTGTGCAAGAACCCCGGTTAGCCCGACCGCTCGCCTTATCCGTTACTATC 2205  
Qy 3428 GTCTTGTAGTCCCAACCGGTAAAGACAGCATTTATCCCACTTGGCAGCAGCACTGGTAAACA 3487





NAME: Fraser, Janis K.	REGISTRATION NUMBER: 34,819	REFERENCE/DOCKET NUMBER: 08191/004002	TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-542-5070	TELEFAX: 617-543-8906	TELEX: 200154	INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:	LENGTH: 4665 base pairs	TYPE: nucleic acid	STRANDEDNESS: double
TOPOLOGY: linear	MOLECULE TYPE: DNA	US-09-169-425C-7	
Query Match	29.7%;	Score 1571.6;	DB 3; Length 4665;
Best Local Similarity	86.3%;	Pred. No. 0;	
Matches 1850;	Conservative	0; Mismatches 114;	Indels 180; Gaps 3;
QY	3008	ACTCAAGGCGGTAATACGGTTATCCACAGATCAGGGGATTAACGAGAAAGACATGT	3067
Db	2624	AATGCATGGCGTATACGGTTATCCACAGATCAGGGGATTAACGAGAAAGACATGT	2565
QY	3068	GAGCAAAAGGCCAGCAAAAGGCCAGGAACCGTAAAGAGCCGGTGTGGGTTTCC	3127
Db	2564	GAGCAAAAGGCCAGCAAAAGGCCAGGAACCGTAAAGAGCCGGTGTGGGTTTCC	2505
QY	3128	ATAGGCTCCGCCCTCGAGGAGCATCAGAAATCGAGCTCAAGTCAGAGGTGCGGAA	3187
Db	2504	ATAGGCTCCGCCCTCGAGGAGCATCAGAAATCGAGCTCAAGTCAGAGGTGCGGAA	2445
QY	3188	ACCCGACAGACTATAAAGATACAGCGGTTTCCCTCGAAGCTCCCTGTCGCTCTC	3247
Db	2444	ACCCGACAGACTATAAAGATACAGCGGTTTCCCTCGAAGCTCCCTGTCGCTCTC	2385
QY	3248	CTGTTCGACCCCTGCGCTTACCGGATACCTGTCCGCTTCTCCCTCGGAGCGTGG	3307
Db	2384	CTGTTCGACCCCTGCGCTTACCGGATACCTGTCCGCTTCTCCCTCGGAGCGTGG	2325
QY	3308	CGCTTTCTATAGTCACTGCTGAGGTATCTCAGTTCGGTGTAGTTCGCTTCCAAAGC	3367
Db	2324	CGCTTTCTATAGTCACTGCTGAGGTATCTCAGTTCGGTGTAGTTCGCTTCCAAAGC	2265
QY	3368	TGGCTGTGTGACGAAACCCCGCTTCAGCCCGACCGCTGCGCTTATCCGTTAACTATC	3427
Db	2264	TGGCTGTGTGACGAAACCCCGCTTCAGCCCGACCGCTGCGCTTATCCGTTAACTATC	2205
QY	3428	GTCTTGAGTCCAAACCCGGTAAGACAGACTTATCGCCACTGGCAGCAGCCACTGGTAACA	3487
Db	2204	GTCTTGAGTCCAAACCCGGTAAGACAGACTTATCGCCACTGGCAGCAGCCACTGGTAACA	2145
QY	3488	GGATTACAGACCGAGGTATGTAGCGGTGCTACAGAGTTCCTGAAAGTGTGGCTTAAC	3547
Db	2144	GGATTACAGACCGAGGTATGTAGCGGTGCTACAGAGTTCCTGAAAGTGTGGCTTAAC	2085
QY	3548	ACGGCTACACTAGAAAGACAGTATTTGGTATCTGCGCTCTGCTGAGCCAGTTACTTCG	3607
Db	2084	ACGGCTACACTAGAAAGACAGTATTTGGTATCTGCGCTCTGCTGAAAGCAGTTACTTCG	2025
QY	3608	GAAAAGAGTTGGTATCTTGTATCCGCAACAAACACCGCTGTGTAGCGGTGTTT	3667
Db	2024	GAAAAGAGTTGGTATCTTGTATCCGCAACAAACACCGCTGTGTAGCGGTGTTT	1965
QY	3668	TGTGTTGCAAGCAGCAGATTAACGCGAGAAAGGATCTCAAGAGATCCTTTGATCT	3727
Db	1964	TGTGTTGCAAGCAGCAGATTAACGCGAGAAAGGATCTCAAGAGATCCTTTGATCT	1905
QY	3728	TTTCTACGGGGTCTGACGCTCAGTGGAAAGGAACTCAGTTAAGGATTTTGGTCATCA	3787
Db	1904	TTTCTACGGGGTCTGACGCTCAGTGGAAAGGAACTCAGTTAAGGATTTTGGTCATCA	1845
QY	3788	GATTATCTCGACCAAGCGCCATCGTGCCT	3819

1844	GATTATCAAAAAGGATCTTTCACCTAGATCTTTTAAATATAAATGAAGTTTAAATCAA	1785
3820	-----CCCACTCTCTGAGTTTGGGG	3840
1784	TCTAAAGTATATATAGTAACCTAGGCTATGGCAGGSCCTTGGCCCGGACGTTGGCTG	1725
3841	GCATGGATGCGCGGATAGCCGCTGCTGTTTCTGGATGCGCAGGATTTGCACCTGCGG	3900
1724	CGAGCCCTGGGCTTACCCGAACTTGGGGGTGGGGTGGGAAAGAAAGAAACGCGG	1665
3901	-----TAGAACTCCGCGAGTCTCCAGCCTCAGGAGCAGCTGAACCAAC	3946
1664	CGTATTGCCCCCAATGGGGTCTCGGTGGGTATCGACAGATGCGCCTGGGACCGAA	1605
3947	TCGCGAGGGGATCGA-----	3961
1604	CCCCCGTTTATGAACAAACGACCAACACCGTGGTTTTATCTCTCTTTTATTGCGG	1545
3962	-----GCCGG	3967
1544	TCATAGCGGGTTCCTTCCGGTATTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT	1485
3968	GCTGGCGAAGAACTCCAGCATGATCCCGCGTGGAGGATCATCCAGCCGGGTCCTCC	4027
1484	GCTGGCGAAGAACTCCAGCATGATCCCGCGTGGAGGATCATCCAGCCGGGTCCTCC	1425
4028	GGAAACGATTCGGAAGCCCAACCTTTTATAGAAGCGCGGTGGGATCGAAATCTCGTG	4087
1424	GGAAACGATTCGGAAGCCCAACCTTTTATAGAAGCGCGGTGGGATCGAAATCTCGTG	1365
4088	ATGCGAGGTTGGCGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	4147
1364	ATGCGAGGTTGGCGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	1305
4148	CTCGTCAAGAGCGGATAGAGCGATGCTGCGAATCGGAGCGCGGATACCGTAAAG	4207
1304	CTCGTCAAGAGCGGATAGAGCGGATGCTGCGAATCGGAGCGCGGATACCGTAAAG	1245
4208	CAGAGGAGCGGTGAGCCCATTCGCGCGCAAGCTCTTTCAGCAATATTCAGGGTAGCAA	4267
1244	CAGAGGAGCGGTGAGCCCATTCGCGCGCAAGCTCTTTCAGCAATATTCAGGGTAGCAA	1185
4268	CGCTATGCTCTGATAGCGTCCGCAACCCAGCGGCGCAGTCCGATGAATCCAGAAA	4327
1184	CGCTATGCTCTGATAGCGTCCGCAACCCAGCGGCGCAGTCCGATGAATCCAGAAA	1125
4328	GCGGCCATTTTCCACCATGATATTCGGCAAGCAGGATCGCCATGGGTTCAGCAGATC	4387
1124	GCGGCCATTTTCCACCATGATATTCGGCAAGCAGGATCGCCATGGGTTCAGCAGATC	1065
4388	CTGCGCGTGGGCAATGCGCGCTTGGCTTGGCTTGGCTTGGCTTGGCTTGGCTTGGCTT	4447
1064	CTGCGCGTGGGCAATGCGCGCTTGGCTTGGCTTGGCTTGGCTTGGCTTGGCTTGGCTT	1005
4448	ATGCTCTTCTGCTCAGATCATCTGATCGAAGACCGGCTTCCATCCGAGTACGTGCTG	4507
1004	ATGCTCTTCTGCTCAGATCATCTGATCGAAGACCGGCTTCCATCCGAGTACGTGCTG	945
4508	CTCATGCGATGTTTTCGCTTGGTGTGATGAGTGGCAGGTAGCCGATCAAGCTATGAG	4567
944	CTCATGCGATGTTTTCGCTTGGTGTGATGAGTGGCAGGTAGCCGATCAAGCTATGAG	885
4568	CCGCGCATTTGCATCAGCCATGATGATGATGATGATGATGATGATGATGATGATGATG	4627
884	CCGCGCATTTGCATCAGCCATGATGATGATGATGATGATGATGATGATGATGATGATG	825
4628	GAGATCTTCCCGGCACTTCGCCCCAATAGCAGCGCTTCCCTTCCCTTCCCTTCCCTT	4687
824	GAGATCTTCCCGGCACTTCGCCCCAATAGCAGCGCTTCCCTTCCCTTCCCTTCCCTT	765
4688	GTCGAGCAGCTGCGCAAGGAAACCGCTGTCGCGCAGCCAGTATGCGCGCTGCTC	4747

Db	764	GTGAGCAGCTCGCGAAGAACGCCCGTGTGGCCAGGCACGATAGCCGCGTGCCTC	705
Qy	4748	GTCTGCAGATTCAATTCAGGGCACCGGACAGGTCGGTCTTCGAAAAAGAACCGGCGCCC	4807
Db	704	GTCTTGCACTTCATTCAGGGCACCGGACAGGTCGGTCTTGAAAAAGAACCGGCGCCCC	645
Qy	4808	CTGGCTGCAGCCGGGAACACGGCGGCATCAGACAGCCGATTGCTGTGTGTGCCAGTC	4867
Db	644	CTGCGCTGACAGCCGGGAACACGGCGGCATCAGACAGCCGATTGCTGTGTGTGCCAGTC	585
Qy	4868	ATAGCCGAATAGCCTCTCCACCAAGCGCGCGAGAACCTGCGTGCATCCATCTGTGTC	4927
Db	584	ATAGCCGAATAGCCTCTCCACCAAGCGCGCGAGAACCTGCGTGCATCCATCTGTGTC	525
Qy	4928	AATCATCGGAAACGATCCTCATCTGCTCTTGATCAGATCTTG	4971
Db	524	AATCATCGGAAACGATCCTCATCTGCTCTTGATCAGATCTTTG	481

RESULT 8  
US-09-759-960-7/c  
; Sequence 7, Application US/09759960  
; Patent No. 6582704  
; GENERAL INFORMATION:  
; APPLICANT: Urban, Robert G.  
; APPLICANT: Chiczo, Roman M.  
; APPLICANT: Collins, Edward J.  
; APPLICANT: Hedley, Mary Lynn  
; TITLE OF INVENTION: IMMUNOGENIC PEPTIDES FROM THE HPV E7  
; TITLE OF INVENTION: PROTEIN  
; NUMBER OF SEQUENCES: 33  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Fish & Richardson, P.C.  
; STREET: 225 Franklin Street

Query Match 29.7%; Score 1571.6; DB 4; Length 4665;  
Best Local Similarity 86.3%; Pred. NO. 0;  
Matches 1850; Conservative 0; Mismatches 114; Indels 180; Gaps 3;

Qy	3008	ACTCAAAGGCGGTAATACGGTTATCCACAGATCAGGGGTAACGCGAGGAAAGAACATGT	3067
Db	2624	AATGCATGGCGGTAATACGGTTATCCACAGATCAGGGGTAACGCGAGGAAAGAACATGT	2565

GENERAL INFORMATION:  
APPLICANT: NATURE TECHNOLOGY CORPORATION, ET AL.  
TITLE OF INVENTION: SELF-ASSEMBLING GENES, VECTORS AND USES THEREOF

NUMBER OF SEQUENCES: 74  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: MUETING, RAASCH & GEBHARDT, P.A.  
STREET: 119 NORTH FOURTH STREET, SUITE 203  
CITY: MINNEAPOLIS  
STATE: MINNESOTA  
COUNTRY: USA  
ZIP: 55401

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/380,190A  
FILING DATE: 26-Aug-1999  
CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/US98/03918  
FILING DATE: 28-FEB-98  
ATTORNEY/AGENT INFORMATION:  
NAME: MUETING, ANN M.  
REGISTRATION NUMBER: 33,977  
REFERENCE/DOCKET NUMBER: 228.00010201  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 612-305-1217  
TELEFAX: 612-305-1228

INFORMATION FOR SEQ ID NO: 26:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 4518 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
SEQUENCE DESCRIPTION: SEQ ID NO: 26:  
US-09-380-190A-26

Query Match 29.7%; Score 1570; DB 4; Length 4518;  
Best Local Similarity 86.2%; Pred. No. 0;  
Matches 1849; Conservative 0; Mismatches 115; Indels 180; Gaps 3;

QY	3968	GGTGGCGAAGAACTCCAGCATGATGCCCGCTGGAGGATCATCCAGCGCGGTCCC	4027
Db	1484	GGTGGCGAAGAACTCCAGCATGATGCCCGCTGGAGGATCATCCAGCGCGGTCCC	1425
QY	4028	GGAAACGATTCGAAAGCCAACTTTTCATAGAGCGCGGTGAATCGAAATCTCGTG	4087
Db	1424	GGAAACGATTCGAAAGCCAACTTTTCATAGAGCGCGGTGAATCGAAATCTCGTG	1365
QY	4088	ATGGCAGGTTGGCGTTCGCTTGGTCGCTCATTTCCAAACCCAGAGTCCCGTTCAGAGAA	4147
Db	1364	ATGGCAGGTTGGCGTTCGCTTGGTCGCTCATTTCCAAACCCAGAGTCCCGTTCAGAGAA	1305
QY	4148	CTGTCGCAAGAGCCATAGAGGCGATCGCTTCGCAATCGGAGCGGCGATACCGTAAAG	4207
Db	1304	CTGTCGCAAGAGCCATAGAGGCGATCGCTTCGCAATCGGAGCGGCGATACCGTAAAG	1245
QY	4208	CACGAGGAGCGGTGAGCCATTCGCCCGCAGCTCTTCAGCAATATCACGGGTAGCCAA	4267
Db	1244	CACGAGGAGCGGTGAGCCATTCGCCCGCAGCTCTTCAGCAATATCACGGGTAGCCAA	1185
QY	4268	CGCTATGCTCATAGCGGTCCGCCACACCCAGCGCGCCACAGTTCGATGAATCCAGAAA	4327
Db	1184	CGCTATGCTCATAGCGGTCCGCCACACCCAGCGCGCCACAGTTCGATGAATCCAGAAA	1125
QY	4328	GCGGCCATTTTCCACCATGATATTCGGCAAGCAGGATCGCCATGGGTCCAGCAGATC	4387
Db	1124	GCGGCCATTTTCCACCATGATATTCGGCAAGCAGGATCGCCATGGGTCCAGCAGATC	1065
QY	4388	CTGCGCGTGGGATCGCGCTTGAGCTGGCGACAGTTCGGCTGGCGCGAGCCCTTG	4447
Db	1064	CTGCGCGTGGGATCGCGCTTGAGCTGGCGACAGTTCGGCTGGCGCGAGCCCTTG	1005
QY	4448	ATGCTCTGCTGCAGATCATCTGATCGACAAGCCGCTTCCATCCGAGTACGTGCTCG	4507
Db	1004	ATGCTCTGCTGCAGATCATCTGATCGACAAGCCGCTTCCATCCGAGTACGTGCTCG	945
QY	4508	CTCGATCGGATGTTTCGCTTGGTTCGAATGGCGAGGTAGCCGGATCAAGCGTATGCAG	4567
Db	944	CTCGATCGGATGTTTCGCTTGGTTCGAATGGCGAGGTAGCCGGATCAAGCGTATGCAG	885
QY	4568	CGCGCGATTCGATCAGCATGATGATCTTTCTGGCAGGAGCAAGTGCATGACAG	4627
Db	884	CGCGCGATTCGATCAGCATGATGATCTTTCTGGCAGGAGCAAGTGCATGACAG	825
QY	4628	GAGATCTGCGCGGCACTTCGCCAATAGCAGCCAGTCCCTTCCCGCTTCAGTGACAAC	4687
Db	824	GAGATCTGCGCGGCACTTCGCCAATAGCAGCCAGTCCCTTCCCGCTTCAGTGACAAC	765
QY	4688	GTGAGCACAGCTGCGCAAGAACCGCCGTGCTGGCCAGCCACGATAGCCCGCTGCTC	4747
Db	764	GTGAGCACAGCTGCGCAAGAACCGCCGTGCTGGCCAGCCACGATAGCCCGCTGCTC	705
QY	4748	GTCTGAGTTCATTCAGGGCACCGGACAGTTCGCTTTGACAAAAGAACCGGCGGCC	4807
Db	704	GTCTGAGTTCATTCAGGGCACCGGACAGTTCGCTTTGACAAAAGAACCGGCGGCC	645
QY	4808	CTGGCTGACAGCGCGAACACCGGGCATCAGAGCAGCGGATGTCTGTGTCGCCAGTC	4867
Db	644	CTGGCTGACAGCGCGAACACCGGGCATCAGAGCAGCGGATGTCTGTGTCGCCAGTC	585
QY	4868	ATAGCCGATAGCTCTCCACCGCGCGGAGACCTCGGTGCAATCCATCTGTTTC	4927
Db	584	ATAGCCGATAGCTCTCCACCGCGCGGAGACCTCGGTGCAATCCATCTGTTTC	525
QY	4928	AATCATGCGAAGCATCTCATCTGCTTCTTGATCAGATCTTG 4971	
Db	524	AATCATGCGAAGCATCTCATCTGCTTCTTGATCAGATCTTG 481	



3068 GAGCAAAAGGCCAGCAAAAGGCCAGCAAAAGGCCAGCTTTTCC 3127  
4235 GAGCAAAAGGCCAGCAAAAGGCCAGCAAAAGGCCAGCTTTTCC 4176  
3128 ATAGGCTCCGCGCCCTGACAGCATCACAAAATCGAGCTCAAGTCAGAGGTGGCGAA 3187  
4175 ATAGGCTCCGCGCCCTGACAGCATCACAAAATCGAGCTCAAGTCAGAGGTGGCGAA 4116  
3188 ACCGACAGGACTATAAAGATACACAGGCGTTTCCCTCGGAAGCTCCCTCGTGCCTCTC 3247  
4115 ACCGACAGGACTATAAAGATACACAGGCGTTTCCCTCGGAAGCTCCCTCGTGCCTCTC 4056  
3248 CTGTTCCGACCTCGCGCTTACCGGATACCTGCGGCTTTCTCCCTCGGAAGCGTGG 3307  
4055 CTGTTCCGACCTCGCGCTTACCGGATACCTGCGGCTTTCTCCCTCGGAAGCGTGG 3996  
3308 CGCTTTCTCATAGCTCAAGCTGAGGTATCTCAGTTCGGTGTAGGTGCTTCCCTCAAGC 3367  
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3935 TGGGCTGTGTGACGAAACCCCGCTTACGCGGACCGCTGCGCTTATCCGCTAACTATC 3876  
3428 GTCTTGAAGTCAACCGGTTAAGACAGCTTATCGGCTGCGCTTATCCGCTAACTATC 3487  
3875 GTCTTGAAGTCAACCGGTTAAGACAGCTTATCGGCTGCGCTTATCCGCTAACTATC 3816  
3488 GANTTAGAGAGGAGTATAGGCGGTGCTACAGAGTCTTGAAGTGGTGCCTTAAT 3547  
3815 GANTTAGAGAGGAGTATAGGCGGTGCTACAGAGTCTTGAAGTGGTGCCTTAAT 3756  
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3755 ACAGCTACACTAGAAACAGTATTTGGTATCTGCGCTGCTGCTGCTGCTGCTGCTGCT 3696  
3608 GAAAAAGAGTTGGTGTAGTCTGTATGCTGCGGCAAAACACACCGCTGCTGAGCGGTGTTT 3667  
3695 GAAAAAGAGTTGGTGTAGTCTGTATGCTGCGGCAAAACACACCGCTGCTGAGCGGTGTTT 3636  
3668 TTGTTTGCAGCAGCAGATTTACGCGGAGAAAAAGGATCTCAAGAGATCTTTGATCT 3727  
3635 TTGTTTGCAGCAGCAGATTTACGCGGAGAAAAAGGATCTCAAGAGATCTTTGATCT 3576  
3728 TTTCTACGCGGTCTGACGCTCAGTGGAAACGAAACTCAAGTAAAGGATTTGTGTATGA 3787  
3575 TTTCTACGCGGTCTGACGCTCAGTGGAAACGAAACTCAAGTAAAGGATTTGTGTATGA 3516  
3788 GATTATCGTCAACAAAGCGGCTATCGTGCCT----- 3819  
3515 GATTATCAAAAGGATCTTACCTAGATCTTTTAAATTAATAAGATTTTAAATCAA 3456  
3820 -----CCCCACTCTGCGAGTTTCGGGG 3840  
3455 TCTAAAGTATATAGTAACCTGAGGTATGCGAGGCGCTGCGCGCCCGAGTGGCTG 3396  
3841 GCATGGATGCGCGATACCGCTGCTGTTTCTTGGATGCGGACGAGATTCACCTGCGG 3900  
3395 CGAGCCCTGGGCTTCAACCGAACTTGGGGGTGGGGTGGGAAAGAAAGAAACGCGGG 3336  
3901 -----TAGAATCTCGGAGGTGCTGAGCTCAGGCTCAGGAGGCTGGAACCAAC 3946  
3335 CGTATTTGCGGCTGCTGCTGCGGTATGACAGAGTGCAGGCTGCGGACCGCTGCGGAC 3276  
3947 TCGCGAGGGATCGA----- 3961  
3275 CCGCGGTTATGAACAAACGACCAACACCGTGGCTTTTATCTGCTTTTATTTGCGG 3216  
3962 -----GCGCGG 3967  
3215 TCATAGCGGGTTCCTTCCGGTATTTGCTCCTTCCGTTTTCAGTTAGCTCCCGCTAG 3156  
3968 GGTGGCGGAGAACTCCAGCATGAGATCCCGGCTGGAGGATCATCCAGCGGCGTCCC 4027

3155 GGTGGCGGAGAACTCCAGCATGAGTCCCGCGCTGGAGGATCATCCAGCGCGCTCCC 3096  
4028 GGAATAAGTTCGGAAGCCCAACCTTTTCATAGAGGCGCGGTGGAATCGAAATCTCGT 4087  
3095 GGAATAAGTTCGGAAGCCCAACCTTTTCATAGAGGCGCGGTGGAATCGAAATCTCGT 3036  
4088 ATGGCAGGTTCGGGCGTCTGCTTTGGTGGTCAATTTGAAACCCAGAGTCCCGCTCAGAANA 4147  
3035 ATGGCAGGTTCGGGCGTCTGCTTTGGTGGTCAATTTGAAACCCAGAGTCCCGCTCAGAANA 2976  
4148 CTGCTCAAGAGGCGATAGAGGCGATGGCTGCGAATCGGAGCGGCGGATACCGTAAAG 4207  
2975 CTGCTCAAGAGGCGATAGAGGCGATGGCTGCGAATCGGAGCGGCGGATACCGTAAAG 2916  
4208 CACGAGGAGGCTCAGCCCATTTCCCGCCCAAGCTCTTCAGCAATATCAACGGGTAGCCAA 4267  
2915 CACGAGGAGGCTCAGCCCATTTCCCGCCCAAGCTCTTCAGCAATATCAACGGGTAGCCAA 2856  
4268 CGCTATGCTCTGATAGCGGTCCGCCACACCCAGCGGCGCACAGTCGATGATCAATCCAGAAA 4327  
2855 CGCTATGCTCTGATAGCGGTCCGCCACACCCAGCGGCGCACAGTCGATGATCAATCCAGAAA 2796  
4328 GCGGCCATTTTCCACCATGATATTGGCAAGCAGCATCGCATGSETCAGACAGATC 4387  
2795 GCGGCCATTTTCCACCATGATATTGGCAAGCAGCATCGCATGSETCAGACAGATC 2736  
4388 CTCGCCGTGGGCGATCGCGCTTGGAGCTTGGCGAAACAGTTCGGCTGGGCGAGCGCTG 4447  
2735 CTCGCCGTGGGCGATCGCTCGCTTGGAGCTTGGCGAAACAGTTCGGCTGGGCGAGCGCTG 2676  
4448 ATGCTCTTCTGTCAGATCATCTGATCGAACAACCGGCTTCCATCCGAGTCTGCTG 4507  
2675 ATGCTCTTCTGTCAGATCATCTGATCGAACAACCGGCTTCCATCCGAGTCTGCTG 2616  
4508 CTCGATGCGATGTTTCTGCTTGGTGGTGGATGGGCGAGTACCGGATCAAGCGTATGCG 4567  
2615 CTCGATGCGATGTTTCTGCTTGGTGGTGGATGGGCGAGTACCGGATCAAGCGTATGCG 2556  
4568 CCGCGCATTTGATGAGCATGATGATATCTTCTCGGCGAGGACAAAGGTGAGATGAC 4627  
2555 CCGCGCATTTGATGAGCATGATGATATCTTCTCGGCGAGGACAAAGGTGAGATGAC 2496  
4628 GAGATCTGCTGCGCGCATCTTGGCGCAATAGAGCAGTCTTCCGCTTCAGTGACAAC 4687  
2495 GAGATCTGCTGCGCGCATCTTGGCGCAATAGAGCAGTCTTCCGCTTCAGTGACAAC 2436  
4688 GTCGAGCAGCTGCGCAAGGAGCGCGCTGTCGCGCAGCCACGATAGCGCGCTGCTC 4747  
2435 GTCGAGCAGCTGCGCAAGGAGCGCGCTGTCGCGCAGCCACGATAGCGCGCTGCTC 2376  
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4808 CTGCGCTGACAGCGGCAACCGCGGCGATCAGAGCAGCGGATGCTTCTGTCGCGCTG 4867  
2315 CTGCGCTGACAGCGGCAACCGCGGCGATCAGAGCAGCGGATGCTTCTGTCGCGCTG 2256  
4868 ATAGCGGATAGCTCTTCCAGCGCGCGGAGAACCTGCTGCAATCCATCTGTTTC 4927  
2255 ATAGCGGATAGCTCTTCCAGCGCGCGGAGAACCTGCTGCAATCCATCTGTTTC 2196  
4928 AATCATGCGAAACGATCT 4971  
2195 AATCATGCGAAACGATCT 2152

RESULT 11  
US-08-751-767A-7/c  
; Sequence 7, Application US/08751767A  
; Patent No. 5954104  
; GENERAL INFORMATION:

APPLICANT: ANDERSON, ROBERT J.  
APPLICANT: GRANT, HUGH  
APPLICANT: MACDONALD, IAN D.  
TITLE OF INVENTION: INTERLUKIN-12 FUSION PROTEIN  
NUMBER OF SEQUENCES: 80  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: NIXON & VANDERHYE P.C.  
STREET: 1100 NORTH GLEBE ROAD  
CITY: ARLINGTON  
STATE: VA  
COUNTRY: USA  
ZIP: 22201  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/751,767A  
FILING DATE: 08-NOV-1996  
CLASSIFICATION: 536  
ATTORNEY/AGENT INFORMATION:  
NAME: SADOFF, B.J.  
REGISTRATION NUMBER: 36,663  
REFERENCE/DOCKET NUMBER: 117-221  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 7038164091  
TELEFAX: 7038164100  
INFORMATION FOR SEQ ID NO: 7:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 6139 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: both  
TOPOLOGY: linear  
MOLECULE TYPE: cdna  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 3222..4841  
US-08-751-767A-7

Query Match 29.7%; Score 1570; DB 2; Length 6139;  
Best Local Similarity 86.2%; Pred. No. 0;  
Matches 1849; Conservative 0; Mismatches 115; Indels 180; Gaps 3;  
QY 3008 ACTCAAGGGGGTAATACGGTTATCCACAGATACAGGGGATAACGACAGGAAAGAAACATGT 3067  
Db 2624 AATGCTATGGCGGTATACGGTTATCCACAGATCAGGGGATAACGACAGGAAAGAAACATGT 2565  
QY 3068 GAGCAAAAGGCCAGCAAAAGGCCAGGAAACCGTAAAGGCCGGTTCTGCTGGCGTTTTC 3127  
Db 2564 GAGCAAAAGGCCAGCAAAAGGCCAGGAAACCGTAAAGGCCGGTTCTGCTGGCGTTTTC 2505  
QY 3128 ATAGGTCGCGCCCTTGACGAGCATCAAAAATCGAGCTCAAGTCAGAGGTGCGGAA 3187  
Db 2504 ATAGGTCGCGCCCTTGACGAGCATCAAAAATCGAGCTCAAGTCAGAGGTGCGGAA 2445  
QY 3188 ACCCGACAGACTATTAAGTACCAGCGTTTCCCTCGAAGCTCCCTCGTGGCTCTC 3247  
Db 2444 ACCCGACAGACTATTAAGTACCAGCGTTTCCCTCGAAGCTCCCTCGTGGCTCTC 2385  
QY 3248 CTGTTCCGACCTGCGCTTACGGATACCTGTCGCTTTCTCCCTTCGGGAGCGTGG 3307  
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QY 3308 CGCTTCTCATAGTCACTGATGTCTCAGTTTCGGTTCAGTTCGTTTCGCTCCAGC 3367  
Db 2324 CGCTTCTCATAGTCACTGATGTCTCAGTTTCGGTTCAGTTCGTTTCGCTCCAGC 2265  
QY 3368 TGGGCTGTGTACAGCAACCCCGCTTCAGCCGACCGCTGCGCTTATCCGGTAATATC 3427  
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Db 2084 ACGGCTACACTAGAAAGACAGTATTTGGTATCTGGCTCTGCTGAAGCAGTTACCTCG 2025  
QY 3608 GAAAAAGAGTTGGTAGCTCTTGTATCCGCAAAACACACCGCTGCTAGCGGTGTTTT 3667  
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QY 3668 TTGTTTGAAGCAGAGATTACGGCAGAAAAAGGATCTCAAGAGATCTTTGATCT 3727  
Db 1964 TTGTTTGAAGCAGAGATTACGGCAGAAAAAGGATCTCAAGAGATCTTTGATCT 1905  
QY 3728 TTCTTACGGGTCTGACGCTCAGTGGAAAGAAACTCAGTTAAGGATTTTGGTCATGA 3787  
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QY 3820 -----CCCCACTCTCGAGTTTCGGG 3840  
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Db 1664 CGTATTGGCCCCAATGGGTCTCGGTGGGTATCGACAGAGTGCACCGCTGGGACCGAA 1605  
QY 3947 TCGGAGGGGATCGA----- 3961  
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QY 3962 -----GCCCGG 3967  
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Db 1304 CTCGTCAAGAGCGCATAGAAGCGCATGCGCTGCGAATCGGAGCGCGCATACCGTAAAG 1245  
QY 4208 CACGAGGAGCGGTGAGCCCATTCGCCCGCAAGCTCTTCAGCAATATCACGGGTAGCCAA 4267  
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QY 4268 CGCTATGTCCTGATAGCGGTCCGACACACCGCGGCAACAGTCGATGAATCCAGAAAA 4327  
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QY 4328 GCGGCAATTTCCACCATGATATTTCGCAAGCAGCATCGCCATCGGTTCAGCAGGATC 4387



Db	1124	CGGGCCATTTTCCACCATGATATTTCGGAAGCAGGATCGGCATCGGATCGAGCAGATC	1065
Qy	4388	CTCCCGCTCGGGCATGCGCGCTTGAGCTTGGCGAAACAGTTTCGGCTGGCGGAGCCCGCTG	4447
Db	1064	CTCCCGCTCGGGCATGCTCGCGCTTGAGCTTGGCGAAACAGTTTCGGCTGGCGGAGCCCGCTG	1005
Qy	4448	ATGCTCTTTCGTCACGATCATCTGATCGACAAAGACCGGCTTCCATCCGAGTACGTCG	4507
Db	1004	ATGCTCTTTCGTCACGATCATCTGATCGACAAAGACCGGCTTCCATCCGAGTACGTCG	945
Qy	4508	CTCGATCGATGTTTCGCTTGGTGTGCAATGGGAGGATAGCCGATCAAGGATGACG	4567
Db	944	CTCGATCGATGTTTCGCTTGGTGTGCAATGGGAGGATAGCCGATCAAGGATGACG	885
Qy	4568	CGCGCGCATTCGATCAGCAGCATGATGGATCTTCTCGGAGGAGCAAGGTGAGATGACG	4627
Db	884	CGCGCGCATTCGATCAGCAGCATGATGGATCTTCTCGGAGGAGCAAGGTGAGATGACG	825
Qy	4628	GAGATCTGCCCCGACATTCGCCCAATAGCAGCAGTCCCTTCCGGTTCAGTGACAC	4687
Db	824	GAGATCTGCCCCGACATTCGCCCAATAGCAGCAGTCCCTTCCGGTTCAGTGACAC	765
Qy	4688	GTGAGCAGATGTCGCGAAGAACCGCCGCTGCTGGCCAGCAGATAGCCGCTGCCTC	4747
Db	764	GTGAGCAGATGTCGCGAAGAACCGCCGCTGCTGGCCAGCAGATAGCCGCTGCCTC	705
Qy	4748	GTCTGTCAGTTTCAATCAGGCGACCGGACAGGTCGCTTTCGCAAAAAGAACCGGGCGCC	4807
Db	704	GTCTGTCAGTTTCAATCAGGCGACCGGACAGGTCGCTTTCGCAAAAAGAACCGGGCGCC	645
Qy	4808	CTGCGTCAGCGCGGAAACACCGCGGCATCAGAGCAGCGATGCTGTTGTGCCAGTC	4867
Db	644	CTGCGTCAGCGCGGAAACACCGCGGCATCAGAGCAGCGATGCTGTTGTGCCAGTC	585
Qy	4868	ATAGCGAATAGCTCTCCACCAAGCGCGCGGAGAACCTGCTGCAATCCATCTTGTTC	4927
Db	584	ATAGCGAATAGCTCTCCACCAAGCGCGCGGAGAACCTGCTGCAATCCATCTTGTTC	525
Qy	4928	AATCATGCGAAACGATCCTCATCTGCTCTTGTGATCAGATCTTG	4971
Db	524	AATCATGCGAAACGATCCTCATCTGCTCTTGTGATCAGATCTTG	481
RESULT 12			
US-09-796-575-4/c			
; Sequence 4, Application US/09796575			
; Patent No. 6632671			
; GENERAL INFORMATION:			
; APPLICANT: Genesegues, Inc.			
; TITLE OF INVENTION: NANOCAPSULE ENCAPSULATION SYSTEM AND METHOD			
; FILE REFERENCE: G332.12-0001			
; CURRENT APPLICATION NUMBER: US/09/796,575			
; CURRENT FILING DATE: 2001-02-28			
; PRIOR APPLICATION NUMBER: US 60/185,282			
; PRIOR FILING DATE: 2000-02-28			
; NUMBER OF SEQ ID NOS: 5			
; SOFTWARE: PatentIn version 3.1			
; SEQ ID NO 4			
; LENGTH: 4748			
; TYPE: DNA			
; ORGANISM: Artificial Sequence			
; FEATURE:			
; OTHER INFORMATION: Provided by Dr. Brett Levay-Young of the University of Minnesota			
US-09-796-575-4			
Query Match 29.7%; Score 1569.8; DB 4; Length 4748;			
Best Local Similarity 86.3%; Pred. No. 0;			
Matches 1847; Conservative 0; Mismatches 112; Indels 180; Gaps 3;			
Qy	3013	AAGCGGGTAATACGGTTATCCACAGATCAGGGGATAACGAGGAAACATGTGAGCA	3072
Db	4744	ATGGCGGTAAATACGGTTATCCACAGATCAGGGGATAACGAGGAAACATGTGAGCA	4685

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Db 3544 ACGATTCCGAAGCCCACTTTCATAGAGGCGGGTGAATCGAAATCTCGTATGCG 3485
QY 4093 AGGTTGGGCGTCCGTTGGTGGTCAATTCGAACCCAGAGTCCGCTCAGAGAACTCGT 4152
Db 3484 AGGTTGGGCGTCCGTTGGTGGTCAATTCGAACCCAGAGTCCGCTCAGAGAACTCGT 3425
QY 4153 CAAGAAGCGATAGAGGCGATCCGCTCGAATCGGAGCGGCGATACGTTAAAGCAGA 4212
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QY 4393 CGTCGGGCATCGCGCTTGAGCTGGGCAACAGTTGGGTGGCGCGAGCCCTGATGCT 4452
Db 3184 CGTCGGGCATCGCGCTTGAGCTGGGCAACAGTTGGGTGGCGCGAGCCCTGATGCT 3125
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Db 3004 GCATTGCATCAGCATGATGGATCTTTCTGGCAGGAGCAAGTGAGATGACAGAGAT 2945
QY 4633 CTGCCCCGGCACTTCGCCCAATAGCAGCAGTCCCTTCCCGCTTCACTGACAAAGTCGA 4692
Db 2944 CTGCCCCGGCACTTCGCCCAATAGCAGCAGTCCCTTCCCGCTTCACTGACAAAGTCGA 2885
QY 4693 GCACAGTGGCAAGGAAACCGCGTCTGGCCAGCCACAGATAGCGGCTGCGCTCGTCCCT 4752
Db 2884 GCACAGTGGCAAGGAAACCGCGTCTGGCCAGCCACAGATAGCGGCTGCGCTCGTCCCT 2825
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QY 4873 CGAATAGCTCTCCACCCAAAGCGCGGAGAACCTGCGTGAATCCATCTGTTCAATCA 4932
Db 2704 CGAATAGCTCTCCACCCAAAGCGCGGAGAACCTGCGTGAATCCATCTGTTCAATCA 2645
QY 4933 TSCGAAACGATCCTCATCTGCTCTTGATCAGATCTTG 4971
Db 2644 TSCGAAACGATCCTCATCTGCTCTTGATCAGATCTTG 2606
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## RESULT 13

US-09-796-575-5/c

; Sequence 5, Application US/09796575

; Patent No. 6632671

; GENERAL INFORMATION:

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; APPLICANT: Geneseq, Inc.
; TITLE OF INVENTION: NANOCAPSULE ENCAPSULATION SYSTEM AND METHOD
; FILE REFERENCE: G332.12-0001
; CURRENT APPLICATION NUMBER: US/09/796,575
; PRIOR FILING DATE: 2001-02-28
; PRIOR APPLICATION NUMBER: US 60/185,282
; PRIOR FILING DATE: 2000-02-28
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 5
; LENGTH: 4992
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Supplied by BD Biosciences Clontech of Palo Alto, California
; US-09-796-575-5
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Query Match 29.7%; Score 1569.8; DB 4; Length 4992;
Best Local Similarity 86.3%; Pred. No. 0;
Matches 1847; Conservative 0; Mismatches 112; Indels 180; Gaps 3;
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Db 4928 AAGCGCAGCAAAAGGCGGACCGGTAAAGGCGGTTGCTGGCGTTTTCATAGG 4869
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Db 4868 CTCGCCCCCTGACGAGCATCACAAAATCGAGCTCAAGTCAGAGTGGCGAAACCG 4809
QY 3193 ACAGGACTAAGATACAGGGGTTTCCCGCTGGAAAGCTCCCTCGCGCTCTCCTGTT 3252
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QY 3493 AGCAGCGAGGTATGTAGCGGTGCTACAGAGTTCCTCAAGTGGTGGCTTAACACGCG 3552
Db 4508 AGCAGCGAGGTATGTAGCGGTGCTACAGAGTTCCTCAAGTGGTGGCTTAACACGCG 4449
QY 3553 TACACTAGAGAACATGATTTGGTATCTGCGCTCTGCTGAAGCCAGTTACCTTCGAAA 3612
Db 4448 TACACTAGAGAACATGATTTGGTATCTGCGCTCTGCTGAAGCCAGTTACCTTCGAAA 4389
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QY	3820	-----CCCCACTCTCGAGTTCGGGGCGATG	3845	Db	3068	GCAGTTTATTCAGGCGCACCGAGGTCGGTCTTTGACAAAAGAAACCGGGCGCCCTGCG	3009
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Db	3968	CGTTTATGAACAAACGACCCACACCGTGGTGTATTTCTGCTTTTATTTGCCGTCATA	3909	RESULT 14			
QY	3962	-----GCCCGGGGTGG	3972	US-08-723-306-6/c			
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Db	3788	ACGATTCGAGCCCACTTTTCATAGAGGCGCGGTGGAATCGAAATCTCGTATGGC	3729	APPLICANT: Morrey PhD, John			
QY	4093	AGTTGGGTGCTTGGTGGTCAATTCGAACCCAGAGTCCCGTCAAGAACTCGT	4152	APPLICANT: Reed, William			
Db	3728	AGTTGGGTGCTTGGTGGTCAATTCGAACCCAGAGTCCCGTCAAGAACTCGT	3669	TITLE OF INVENTION: Cassette for Expression of Lytic			
QY	4153	CAAGAAGCGGATAGAGGCGATCGCTGCGAATCGGGAGCGGCGATACCGTAAGCACGA	4212	TITLE OF INVENTION: Peptides in Mammalian Transgenic Organisms			
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Db	3608	GGAAGCGGTAGCGCATTCGCGCCAGCTCTTCAGCAATATCAGGGTAGCCACGCTA	3549	ADDRESSEE: Trask Britt and Rossa			
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Db	3548	TGTCCTGATAGCGGTCCGCCACACCCAGCGGCCACAGTCGATGAATCCAGAAAGCGGC	3489	CITY: Salt Lake City			
QY	4333	CATTTCCACATGATATTCGGCAAGCAGGATCGCCATGGTCACGACGAGATCCTCGC	4392	STATE: Utah			
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QY	4393	CGTCGGGATCGCGCTTGAGCTGGCAACAGTTCGGCTGGCGCGAGCCCTGATGCT	4452	COUNTRY: USA			
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QY	4513	TGCGATGTTTCTGTTGTTGATAGGCGAGTAGCCGATCAAGCGTATGACGCCGC	4572	OPERATING SYSTEM: PC-DOS/MS-DOS			
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Db	3188	CCTGCCCGGCACTTCGCCCAATAGCAGCGAGTCCCTCCCGCTTCAGTGCAAGCTGCA	3129	ATTORNEY/AGENT INFORMATION:			
QY	4693	GCACAGCTGCGCAAGGAAGCCCGTCTGGCCAGCCACGATAGCGCGCTGCTCGTCT	4752	NAME: Sweigert PhD, Susan E			
				REGISTRATION NUMBER: 36,289			
				REFERENCE/DOCKET NUMBER: 2549			
				TELECOMMUNICATION INFORMATION:			
				TELEPHONE: 8015321922			
				TELEFAX: 8015319168			
				INFORMATION FOR SEQ ID NO: 6:			
				SEQUENCE CHARACTERISTICS:			
				LENGTH: 8797 base pairs			
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				MOLECULE TYPE: other nucleic acid			
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				DESCRIPTION: taurin beta casein 5' regulatory region plus genes encoding			
				DESCRIPTION: amphipathic peptide and green fluorescent protein"			
				HYPOTHETICAL: YES			
				ANTI-SENSE: NO			
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				Matches 1847; Conservative			
				29.7%; Score 1569.8; DB 2; Length 8797;			
				Pred. No. 0; Mismatches 112; Indels 180; Gaps 3;			
				QY 3013 AAGCGGTAAATACGCTTATCCACAGATCAGGGGATAACGAGGAAACATGTGAGCA 3072			

Db	8793	ATGGCGGTAAATACGGTTATCCACAGATCAGGGGATAACGACGAGAAAGAACATGTGAGCA	8734	7713	GCGCGGTTCCCTTCGGGTATTGTTCTCTTCCCTTCCGTTTTCAGTTAGCTCCCTCCTAGGTTGG	7654
QY	3073	AAAGCCAGCAAAAGGCGAGAACCGTAAAGAGGCGCGTTCTGCGCTTTTTCATAGG	3132	3973	GCGAAGAACTCCAGCATGAGATCCCGCGCTGGAGATCATCCAGCGCGCTCCCGAAA	4032
Db	8733	AAAGCCAGCAAAAGGCGAGAACCGTAAAGAGGCGCGTTCTGCGCTTTTTCATAGG	8674	7653	GCGAAGAACTCCAGCATGAGATCCCGCGCTGGAGATCATCCAGCGCGCTCCCGAAA	7594
QY	3133	CTCCGCGCCCTTGACGAGCATCACAAAATCGACGCTCAAGTCAGAGTGGCGAAACCGG	3192	4033	ACGATTCGGAAGCCCAACCTTTTCATAGAGGCGCGGTGGAAATCGAAATCTCGTATGGC	4092
Db	8673	CTCCGCGCCCTTGACGAGCATCACAAAATCGACGCTCAAGTCAGAGTGGCGAAACCGG	8614	7593	ACGATTCGGAAGCCCAACCTTTTCATAGAGGCGCGGTGGAAATCGAAATCTCGTATGGC	7534
QY	3193	ACAGGACTATAAGATACACAGCGCTTTCCCTGGAAGCTCCCTCGCGCTTCTCTGT	3252	4093	AGTTTGGCGTGGCTTGGTTCGTCATTTTCGAACCCAGAGTCCCGCTCAGAAGAACTCGT	4152
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QY	3253	CGACCTTGGCGCTTACCGGATACCTGTCGCGCTTTCTCCCTTCGGGAAGCGTGGCGTT	3312	4153	CAAGAAGCGGATAGAGCGGATCGCTCGGAATCGGGAGCGCGATACCGTAAAGACGA	4212
Db	8553	CGACCTTGGCGCTTACCGGATACCTGTCGCGCTTTCTCCCTTCGGGAAGCGTGGCGTT	8494	7473	CAAGAAGCGGATAGAGCGGATCGCTCGGAATCGGGAGCGCGATACCGTAAAGACGA	7414
QY	3313	TCTCATAGCTACAGCTGTAGGTATCTCAGTTTCGGTGTAGGTGCTTCGCTCAAGCTGGC	3372	4213	GGAGCGGTACAGCCCATTCGCGCCCAAGCTCTTCAGCAATATCAGGGTAGCCACGCTA	4272
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QY	3373	TGTGTGACAGAACCCCGTTTTCAGCCGACCGCTCGCGCTTATCCGGTAACTATCGTCTT	3432	4273	TGTCTGTATAGCGTTCGCCACACCCAGCCGCGCCACAGTCCGATGAATCCAGAAAGCGC	4332
Db	8433	TGTGTGACAGAACCCCGTTTTCAGCCGACCGCTCGCGCTTATCCGGTAACTATCGTCTT	8374	7353	TGTCTGTATAGCGTTCGCCACACCCAGCCGCGCCACAGTCCGATGAATCCAGAAAGCGC	7294
QY	3433	GAGTCCAAACCCGGTAAGACAGACTTATCGCACTGGCAGAGCCACTGGTAACAGGATT	3492	4333	CATTTTCCACCATGATATTCGGCAAGCAGGATCGCATGGGTCAAGCAGAGTCTCTCGC	4392
Db	8373	GAGTCCAAACCCGGTAAGACAGACTTATCGCACTGGCAGAGCCACTGGTAACAGGATT	8314	7293	CATTTTCCACCATGATATTCGGCAAGCAGGATCGCATGGGTCAAGCAGAGTCTCTCGC	7234
QY	3493	AGCAGAGCAGGTATGTAGGCGGTGTACAGAGTTCTTGAAGTGGTGGCCTTAACTACGGC	3552	4393	CGTCGGCATGCGCGCTTGAAGCTTGGCTGGCGCGAGCCCTGATGCT	4452
Db	8313	AGCAGAGCAGGTATGTAGGCGGTGTACAGAGTTCTTGAAGTGGTGGCCTTAACTACGGC	8254	7233	CGTCGGCATGCTCGCTTGAAGCTTGGCTGGCGCGAGCCCTGATGCT	7174
QY	3553	TACACTAGAAAGAACAGTATTTGGTATCTCGCTCTGCTGAAAGCAGTTACCTTCGGA	3612	4453	CTTCGTCCAGATCATCTGATTCGCAAGACCGGCTTCCATCCGAGTACGTCCTCGTCA	4512
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QY	3613	AGAGTTGGTATCTTGCATCGGCAAAACAAACCCGCTGGTAGCGGTGGTTTTTTGTT	3672	4513	TGGATCTTTTGGTGGTTCGAAATGGGAGGTAGCGGATCAAGCGTATGACGCGCC	4572
Db	8193	AGAGTTGGTATCTTGCATCGGCAAAACAAACCCGCTGGTAGCGGTGGTTTTTTGTT	8134	7113	TGGATCTTTTGGTGGTTCGAAATGGGAGGTAGCGGATCAAGCGTATGACGCGCC	7054
QY	3673	TGCAAGCAGCAGATACCGCAGAAAGAAAGGATCTCAAGAGATCTTTTGAATCTTTCT	3732	4573	GCATTCATCAGCATGATGATGATCTTTCGCGAGAGCAAGTGGAGTACAGAGAGAT	4632
Db	8133	TGCAAGCAGCAGATACCGCAGAAAGAAAGGATCTCAAGAGATCTTTTGAATCTTTCT	8074	7053	GCATTCATCAGCATGATGATGATCTTTCGCGAGAGCAAGTGGAGTACAGAGAGAT	6994
QY	3733	ACGGGTCTGACGCTCAGTGGAAACGAAACTCAGCTTAAAGGATTTTGGTCATGAGATTA	3792	4633	CTTCGCGCGCACTTCGCGCAATAGCAGCCAGTCCCTTCCCGCTTCAAGTCAACGTCGA	4692
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QY	3846	GATCGCGGATACCGGTGCTGCTTTTCTGGATGCGGACGATTTGCACTGCGCG	3900	4813	CTGACAGCGGAAACACGGCGGATCAGAGCAGCCGATTCGTTGTTGTTGCGCAGTATAGC	4872
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QY	3901	-----TAGAACTCCGGAGGTGCTCAGCCTCAGGAGCAGTGAACCAACTCGCG	3951	4873	CGAATAGCTCTCCACCGGCGGAGAACCTGCGTGAATCCATCTTGTTCATCA	4932
Db	7833	TGGCCCAATGGGTCTCGTGGGGTATCGACAGAGTGGCCCTGGGACCGAACCCCG	7774	6753	CGAATAGCTCTCCACCGGCGGAGAACCTGCGTGAATCCATCTTGTTCATCA	6694
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RESULT 15

PCT-US96-10041-6/c

QY	3373	TGTGTGACGAAACCCCGCTTTCAGCCCGACCGCTGCGCTTATCCGGTAACCTATCGTCTT	3432
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Db	8013	TCAAAAGGATCTTACCTAGATCTTTTAAATTAAGATTTTAAATCAATCTAA	7954
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Db	7953	AGTATATAGTAACCTGAGGCTATGCGAGGCGCTGCGCCCGACGTTGGCTGCGAGC	7894
QY	3846	GATGCGCGATAGCCGCTGCTGTTTCCTGGATGCGCAGCGGATTTGCATGCGCG	3900
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Db	7773	CGTTTATGAACAAACGACCAACACCGTGGCTTTTATCTGCTTTTATTTGCGGTCTA	7714
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Sequence 6, Application PC/TUS9610041  
GENERAL INFORMATION:  
APPLICANT: White PhD, Kenneth  
APPLICANT: Morrey PhD, John  
APPLICANT: Reed, William  
TITLE OF INVENTION: Cassette for Expression of Lytic Peptides in Mammalian Transgenic Organisms  
NUMBER OF SEQUENCES: 32  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Trask Britt and Rossa  
STREET: P.O. Box 2550  
CITY: Salt Lake City  
STATE: Utah  
COUNTRY: USA  
ZIP: 84110  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: PCT/US96/10041  
FILING DATE:  
CLASSIFICATION:  
ATTORNEY/AGENT INFORMATION:  
NAME: Sweigert PhD, Susan E  
REGISTRATION NUMBER: 36,289  
REFERENCE/DOCKET NUMBER: 2549  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 8015321922  
TELEFAX: 8015319168  
INFORMATION FOR SEQ ID NO: 6:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 8797 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: not relevant  
MOLECULE TYPE: other nucleic acid  
DESCRIPTION: /desc = "Construct comprising Bos taurus beta casein 5' regulatory region plus genes encoding amphipathic peptide and green fluorescent protein"  
HYPOTHETICAL: YES  
ANTI-SENSE: NO  
PCT-US96-10041-6

Query Match 29.7%; Score 1569.8; DB 5; Length 8797;  
Best Local Similarity 86.3%; Pred. No. 0;  
Matches 1847; Conservative 0; Mismatches 112; Indels 180; Gaps 3;

QY	3013	AAGCGGTAATACGGTTATCCACAGATCAGGGGATACCGAGGAAAGACATGTGACCA	3072
Db	8793	ATGGCGGTAATACGGTTATCCACAGATCAGGGGATACCGAGGAAAGACATGTGACCA	8734
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QY	3193	ACAGGACTATAAGATACAGGCGTTCCCTCGGAGACTCCCTGTCGCTCTCCCTGT	3252
Db	8613	ACAGGACTATAAGATACAGGCGTTCCCTCGGAGACTCCCTGTCGCTCTCCCTGT	8554
QY	3253	CCGACCTCGCGCTTACCGGATACCTGTCGCGCTTCCTCCCTTCGGGAAGCGTGGCGCT	3312
Db	8553	CCGACCTCGCGCTTACCGGATACCTGTCGCGCTTCCTCCCTTCGGGAAGCGTGGCGCT	8494
QY	3313	TCTCATAGCTCAGCGTGTAGGTATCTCAGTTGGTGTAGGTTCGCTCAAGCTGGC	3372
Db	8493	TCTCATAGCTCAGCGTGTAGGTATCTCAGTTGGTGTAGGTTCGCTCAAGCTGGC	8434

[illegible]

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GenCore version 5.1.1.6  
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Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

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Published Applications NA:\*

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- 2: /cgn2\_6/ptodata/1/pubpna/PCT\_NEW\_PUB.seq:\*
- 3: /cgn2\_6/ptodata/1/pubpna/US06\_NEW\_PUB.seq:\*
- 4: /cgn2\_6/ptodata/1/pubpna/US06\_PUBCOMB.seq:\*
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- 6: /cgn2\_6/ptodata/1/pubpna/PCTUS\_PUBCOMB.seq:\*
- 7: /cgn2\_6/ptodata/1/pubpna/US08\_NEW\_PUB.seq:\*
- 8: /cgn2\_6/ptodata/1/pubpna/US08\_PUBCOMB.seq:\*
- 9: /cgn2\_6/ptodata/1/pubpna/US09A\_PUBCOMB.seq:\*
- 10: /cgn2\_6/ptodata/1/pubpna/US09B\_PUBCOMB.seq:\*
- 11: /cgn2\_6/ptodata/1/pubpna/US09C\_PUBCOMB.seq:\*
- 12: /cgn2\_6/ptodata/1/pubpna/US09\_NEW\_PUB.seq:\*
- 13: /cgn2\_6/ptodata/1/pubpna/US09\_NEW\_PUB.seq:\*
- 14: /cgn2\_6/ptodata/1/pubpna/US10A\_PUBCOMB.seq:\*
- 15: /cgn2\_6/ptodata/1/pubpna/US10B\_PUBCOMB.seq:\*
- 16: /cgn2\_6/ptodata/1/pubpna/US10C\_PUBCOMB.seq:\*
- 17: /cgn2\_6/ptodata/1/pubpna/US10\_NEW\_PUB.seq:\*
- 18: /cgn2\_6/ptodata/1/pubpna/US60\_NEW\_PUB.seq:\*
- 19: /cgn2\_6/ptodata/1/pubpna/US60\_PUBCOMB.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	5283	100.0	5283	11	US-09-921-143-36
2	2240	42.4	8349	15	US-10-198-478-16
3	1793.4	33.9	4800	15	US-10-322-360-1
4	1692.4	32.0	5225	15	US-10-286-186-16
5	1632.8	30.9	5285	14	US-10-038-001-1
6	1603.8	30.4	2192	15	US-10-021-403A-10
7	1603.8	30.4	3534	13	US-10-359-919A-11
8	1603.8	30.4	3534	13	US-10-359-919A-12
9	1603.8	30.4	3534	13	US-10-359-919A-13
10	1603.8	30.4	3534	13	US-10-359-919A-14
11	1603.8	30.4	3534	13	US-10-315-907A-11
12	1603.8	30.4	3534	13	US-10-315-907A-15
13	1603.8	30.4	3534	13	US-10-315-907A-11
14	1603.8	30.4	3534	13	US-10-315-907A-12
15	1603.8	30.4	3534	13	US-10-315-907A-13

15	1603.8	30.4	3534	13	US-10-315-907A-14	Sequence 14, Appl
16	1603.8	30.4	3534	13	US-10-315-907A-15	Sequence 15, Appl
17	1603.8	30.4	3534	13	US-10-021-403A-9	Sequence 9, Appl
18	1603.8	30.4	3534	16	US-10-395-709-11	Sequence 11, Appl
19	1603.8	30.4	3534	16	US-10-395-709-12	Sequence 12, Appl
20	1603.8	30.4	3534	16	US-10-395-709-13	Sequence 13, Appl
21	1603.8	30.4	3534	16	US-10-395-709-14	Sequence 14, Appl
22	1603.8	30.4	3534	16	US-10-395-709-15	Sequence 15, Appl
23	1603.8	30.4	3534	17	US-10-619-939-1	Sequence 14, Appl
24	1603.8	30.4	3534	17	US-10-281-067B-11	Sequence 11, Appl
25	1603.8	30.4	3534	17	US-10-281-067B-12	Sequence 12, Appl
26	1603.8	30.4	3534	17	US-10-281-067B-13	Sequence 13, Appl
27	1603.8	30.4	3534	17	US-10-281-067B-14	Sequence 14, Appl
28	1603.8	30.4	3534	17	US-10-281-067B-15	Sequence 15, Appl
29	1603.8	30.4	3599	13	US-09-861-101-3	Sequence 26, Appl
30	1603.4	30.4	3558	17	US-10-281-067B-26	Sequence 2, Appl
31	1602.2	30.3	3600	13	US-09-861-101-2	Sequence 3, Appl
32	1600	30.3	5966	15	US-10-136-837-3	Sequence 2, Appl
33	1571.6	29.7	4665	9	US-09-759-960-7	Sequence 3, Appl
34	1570	29.7	4886	15	US-10-128-853-4	Sequence 7, Appl
35	1570	29.7	5031	15	US-10-033-717-9	Sequence 4, Appl
36	1570	29.7	5054	15	US-10-033-717-8	Sequence 9, Appl
37	1570	29.7	5130	15	US-10-033-717-7	Sequence 8, Appl
38	1570	29.7	5168	15	US-10-033-717-5	Sequence 7, Appl
39	1569.8	29.7	4151	13	US-10-421-285-15	Sequence 5, Appl
40	1569.8	29.7	4692	15	US-10-161-403-29	Sequence 15, Appl
41	1569.8	29.7	4692	17	US-10-433-640-16	Sequence 29, Appl
42	1569.8	29.7	4727	15	US-10-115-987B-12	Sequence 16, Appl
43	1569.8	29.7	4733	10	US-09-797-496B-1	Sequence 12, Appl
44	1569.8	29.7	4733	15	US-10-177-390-1	Sequence 1, Appl
45	1569.8	29.7	4740	15	US-10-115-987B-13	Sequence 13, Appl

#### ALIGNMENTS

RESULT 1  
US-09-921-143-36  
; Sequence 36, Application US/09921143  
; Publication No. US20030215921A1  
; GENERAL INFORMATION:  
; APPLICANT: Coleman, Timothy  
; TITLE OF INVENTION: Vascular Endothelial Growth Factor-2  
; FILE REFERENCE: PFI12P6  
; CURRENT APPLICATION NUMBER: US/09/921,143  
; CURRENT FILING DATE: 2001-08-03  
; PRIOR APPLICATION NUMBER: 60/223,276  
; PRIOR FILING DATE: 2000-08-04  
; NUMBER OF SEQ ID NOS: 36  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 36  
; LENGTH: 5283  
; TYPE: DNA  
; ORGANISM: homo sapiens  
US-09-921-143-36

Query Match 100.0%; Score 5283; DB 11; Length 5283;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 5283; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
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QY 4266 AAGCTATGCTCTGATAGCGGTGCGGCACACCCAGCGGCGACAGTGCATGAATCCAGAA 4325
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QY 7327 AAGCTATGCTCTGATAGCGGTGCGGCACACCCAGCGGCGACAGTGCATGAATCCAGAA 7386
QY 4326 AAGCGGCCATTTTCCACCATGATATTCGCAAGCAGCATCGCATGGGTACGACGAGA 4385
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QY 5166 GTCAGATAGCCAGTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCT 5225
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## RESULT 3

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US-10-322-360-1/c
; Sequence 1, Application US/10322360
; Publication No. US20030165946A1
; GENERAL INFORMATION:
; APPLICANT: Evans, Glen A.
; TITLE OF INVENTION: A Method for the Complete Chemical
; FILE REFERENCE: P-EA 5511
; CURRENT APPLICATION NUMBER: US/10/322,360
; PRIOR FILING DATE: 2002-12-17
; PRIOR APPLICATION NUMBER: US 09/554,929
; NUMBER OF SEQ ID NOS: 193
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 4800
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic plasmid
US-10-322-360-1
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Query Match 33.9%; Score 1793.4; DB 15; Length 4800;
Best Local Similarity 91.8%; Pred. No. 0;
Matches 1980; Conservative 0; Mismatches 1; Indels 176; Gaps 1;
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Db |||||
QY 3187 AACCCGACAGACTATAAGATACAGGCTTCCCTCGAAGCTCCCTCGTGGGCTCT 3246
Db |||||
QY 4740 AACCCGACAGACTATAAGATACAGGCTTCCCTCGAAGCTCCCTCGTGGGCTCT 4681
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QY 3247 CCGTTCGACCTCGCGCTTACCGGATACCTGTCCGCTTCTCCCTTCGGGAAGCGTG 3306
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Db	4620	GGCGTTCTCTATAGTCACTGCTAGTATCTAGTTCCGGTGTAGTTCGGTCCGCTC	4561	Db	3716	CCTCGCGTGGGCGATCGCGCTTGGAGCTTGGCGAAACAGTTTCGGCTGGCGAGCCCT	3657
Qy	3367	CTGGCTGTGTGACGAAACCCCGCTTCAGCCCGACCGCTGCGCTTATCCGGTAACAT	3426	Qy	4447	GATGCTCTTCTCGATGATCATCTGATCGAACAACCGGCTTCCATCCGAGTACGTGCTC	4506
Db	4560	CTGGCTGTGTGACGAAACCCCGCTTCAGCCCGACCGCTGCGCTTATCCGGTAACAT	4501	Db	3656	GATGCTCTTCTCGATGATCATCTGATCGAACAACCGGCTTCCATCCGAGTACGTGCTC	3597
Qy	3427	CGTCTTGAAGTCCAAACCCCGCTTAAGACACGACTTATCGCCACTGGCAGCAGCTGTAAC	3486	Qy	4507	GCTCGATCGATGTTTCGCTTGGTGGTGAATGGCAGGTAGCGGATCAAGCGTATGCA	4566
Db	4500	CGTCTTGAAGTCCAAACCCCGCTTAAGACACGACTTATCGCCACTGGCAGCAGCTGTAAC	4441	Db	3596	GCTCGATCGATGTTTCGCTTGGTGGTGAATGGCAGGTAGCGGATCAAGCGTATGCA	3537
Qy	3487	AGGATTACAGACGAGTATGAGCGGTGCTACAGAGTTCTTCAAGTGGTGGCTTAAC	3546	Qy	4567	GCCTCGCATTTGATCAGCCATGATGATATCTTTCGCGCAGGAGCAAGGTGAGTACACA	4626
Db	4440	AGGATTACAGACGAGTATGAGCGGTGCTACAGAGTTCTTCAAGTGGTGGCTTAAC	4381	Db	3536	GCCTCGCATTTGATCAGCCATGATGATATCTTTCGCGCAGGAGCAAGGTGAGTACACA	3477
Qy	3547	TACGCTTACACTAGAGAAACAGTATTTGGTATCTCGCTCTGCTGAAGCAGTTACCTTC	3606	Qy	4627	GGAGATCTCTGCTCCCGCACTTTCGCTTGAAGCAGTCCCTTCCCGCTTCCAGTGACAA	4686
Db	4380	TACGCTTACACTAGAGAAACAGTATTTGGTATCTCGCTCTGCTGAAGCAGTTACCTTC	4321	Db	3476	GGAGATCTCTGCTCCCGCACTTTCGCTTGAAGCAGTCCCTTCCCGCTTCCAGTGACAA	3417
Qy	3607	GGAAAAAGATTGGTAGCTCTTGGATCCGGCAAAACAAACACCGCTGGTACCGTGTGTTT	3666	Qy	4687	CGTCAGACACAGTCTGGCAAGAAACCGCGCTGTCGCCAGCCACGATAGCCGCGCTGCCT	4746
Db	4320	GGAAAAAGATTGGTAGCTCTTGGATCCGGCAAAACAAACACCGCTGGTACCGTGTGTTT	4261	Db	3416	CGTCAGACACAGTCTGGCAAGAAACCGCGCTGTCGCCAGCCACGATAGCCGCGCTGCCT	3357
Qy	3667	TTTGTTCAGACGACAGTATGAGCGGATACGGCAGAAAAAGGATCTCAAGAGATCTTTGATC	3726	Qy	4747	CGTCTGCGATTTCAATTCAGGGCACCGGACAGCTCGTCTTGAACAAAGAAACCGGCGCC	4806
Db	4260	TTTGTTCAGACGACAGTATGAGCGGATACGGCAGAAAAAGGATCTCAAGAGATCTTTGATC	4201	Db	3356	CGTCTGCGATTTCAATTCAGGGCACCGGACAGCTCGTCTTGAACAAAGAAACCGGCGCC	3297
Qy	3727	TTTTCACGGGTCTGACGCTCAGTGGAAACGAAACCTCAGTTAAGGATTTTGGTCAAG	3786	Qy	4807	CCTGCGCTGACAGCGGAAACACGGCGGATCAGAGCAGCGGATTCGCTGTCGCTTGTG	4866
Db	4200	TTTTCACGGGTCTGACGCTCAGTGGAAACGAAACCTCAGTTAAGGATTTTGGTCAAT	4142	Db	3296	CCTGCGCTGACAGCGGAAACACGGCGGATCAGAGCAGCGGATTCGCTGTCGCTTGTG	3237
Qy	3787	AGATTATGTCGACAAAGGGGCGATCGTGCTCCCTCCCTGCTGCTGCTGCTGCTGCTG	3846	Qy	4867	CATAGCGAATAGCTCTCCACCAAGCGCGGAGAACTGCTGCTGCTGCTGCTGCTGCTG	4926
Db	4141	-----	4142	Db	3236	CATAGCGAATAGCTCTCCACCAAGCGCGGAGAACTGCTGCTGCTGCTGCTGCTGCTG	3177
Qy	3847	ATCGCGGATAGCGCTGCTGCTTCTGATGCGCGAGGATTTGACATCCCGGTAGAAC	3906	Qy	4927	CAATCATGGAACGATCTCTCTGATCAGATCTGATCAGATCTGATCAGATCTGATCAG	4986
Db	4141	-----	4142	Db	3176	CAATCATGGAACGATCTCTCTGATCAGATCTGATCAGATCTGATCAGATCTGATCAG	3117
Qy	3907	TCCGCGAGTGTCTCCAGCTCAGGACAGCTGAAACAACTCCGAGGGGATCGAGCCG	3966	Qy	4987	AGATCTCTGCGCGCAAGAACCCATCCAGTTTACTTTCAGAGCTTCCCAACCTTACAG	5046
Db	4141	-----	4137	Db	3116	AGATCTCTGCGCGCAAGAACCCATCCAGTTTACTTTCAGAGGCTTCCCAACCTTACAG	3057
Qy	3967	GGGTGGCGAAGAACTCCAGATGAGATCCCGGCTGGAGGATCCTCCAGCGCGCTCC	4026	Qy	5047	AGGCGCGCCAGCTGCAATTCGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	5106
Db	4136	GGGTGGCGAAGAACTCCAGATGAGATCCCGGCTGGAGGATCCTCCAGCGCGCTCC	4077	Db	3056	AGGCGCGCCAGCTGCAATTCGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	2997
Qy	4027	CGGAAACGATTCGGAAGCCCACTTTCATAGAGCGCGGCTGGAATCGAAATCTCGT	4086	Qy	5107	ATCGCCATGTAAGCCCACTGCAAGCTACCTGCTTCTTTCGCTGCTGCTGCTGCTGCTG	5166
Db	4076	CGGAAACGATTCGGAAGCCCACTTTCATAGAGCGCGGCTGGAATCGAAATCTCGT	4017	Db	2996	ATCGCCATGTAAGCCCACTGCAAGCTACCTGCTTCTTTCGCTGCTGCTGCTGCTGCTG	2937
Qy	4087	GATGGCAGTTGGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	4146	Qy	5167	TCCAGATAGCCAGTACGATCAGATTCATCCGGGTGAGCAGCTTCTGCGGATCGGCTT	5226
Db	4016	GATGGCAGTTGGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	3957	Db	2936	TCCAGATAGCCAGTACGATCAGATTCATCCGGGTGAGCAGCTTCTGCGGATCGGCTT	2877
Qy	4147	ACTCGTCAAGAGCGGATAGAGGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	4206	Qy	5227	TCTACGTGTTCCGCTTCTTTCAGAGCGCTTTCGCGCTTTCGCGCTTTCGCGGAGCGTG	5283
Db	3956	ACTCGTCAAGAGCGGATAGAGGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	3897	Db	2876	TCTACGTGTTCCGCTTCTTTCAGAGCGCTTTCGCGCTTTCGCGCTTTCGCGGAGCGTG	2820
Qy	4207	GCACGAGAGCGGTACAGCCCTTCCGCGCAAGCTTTCAGCAATATCAGGGTAGCCA	4266				
Db	3896	GCACGAGAGCGGTACAGCCCTTCCGCGCAAGCTTTCAGCAATATCAGGGTAGCCA	3837				
Qy	4267	AGCTATGCTCTGATAGCGGTCCGCGCAACCGCGCGGACAGTTCGATGATCAGAAA	4326				
Db	3836	AGCTATGCTCTGATAGCGGTCCGCGCAACCGCGCGGACAGTTCGATGATCAGAAA	3777				
Qy	4327	AGCGGCATTTTCCACCATGATATTCGCGCAGCGGATCGCCATGGGTTCACGACGAGAT	4386				

RESULT 4  
US-10-286-186-16/c  
; Sequence 16, Application US/10286186  
; Publication No. US20030143741A1  
; GENERAL INFORMATION:  
; APPLICANT: PALMER, KENNETH E.  
; APPLICANT: POGUE, GARY P.  
; TITLE OF INVENTION: ROLLING CIRCLE REPLICON EXPRESSION  
; TITLE OF INVENTION: VECTOR  
; FILE REFERENCE: 008010179000US00







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QY 3926 ---TCAGGAGCAGCTGAACCACTCGCGAGGGATCGAGCCGGGCTGGGCGAAGAACT 3982
Db 4145 GGGTCACGTGCTCCGGACCAACCGCGGAAGTGGTCTCCACGAAGTCCCGGAGAAC 4086
QY 3983 CAGCATGAGATCCCGGCTGGAGGATCATCCAGCCGGCGTCCCGGAAACGATTCCGA 4042
Db 4085 CGAGCGGTGGTCCAGAACTCGACCGCTCCGGGACGTCGCGCGGTGAGCACCGGAA 4026
QY 4043 AGCCCAACCTTTCATAGAAAGGGCGGTGGAAATCGAAATCTCGTATGACGAGTTGGCG 4102
Db 4025 CGGCACTGGTCAACTTGGCCATGGTGGCCCTCTCACGTGCTATTATTGAAGCAATTATC 3966
QY 4103 TCGTTGTGTCGGTCAATTTCGAACCCCGAGAGTCCCG----- 4137
Db 3965 AGGGTTATTGTTCTATGAGCGGATACATATTTGAATGATTTAGAAAAATAACAAATAG 3906
QY 4138 ----- 4137
Db 3905 GGGTTCGCGGCACATTTCCCGGAAAAGTGCCACCTGTATGGGTGTGAATACGCCACAG 3846
QY 4138 -----CTCAGAGAACTC 4150
Db 3845 ATGGTAAAGAGAAAAATACCGCATCAGGAAATTGTAGCGTTAATAATTACAGAAACTC 3786
QY 4151 GTCAGAGAGCGATAGAAAGCGATGCGCTGCGAATCGGGAGCGGCGATACCGTAAAGCAC 4210
Db 3785 GTCAGAGAGCGATAGAAAGCGATGCGCTGCGAATCGGGAGCGGCGATACCGTAAAGCAC 3726
QY 4211 GAGAAAGCGTACGCCATTCCGCGCCCAAGCTCTTTCAGCAATATCACGGGTAGCCAAAGC 4270
Db 3725 GAGAAAGCGTACGCCATTCCGCGCCCAAGCTCTTTCAGCAATATCACGGGTAGCCAAAGC 3666
QY 4271 TATGTCCTGATAGCGTCCGCGCACCCAGCGCGGCCACAGTCGATGAATCCAGAAAAGCG 4330
Db 3665 TATGTCCTGATAGCGTCCGCGCACCCAGCGCGGCCACAGTCGATGAATCCAGAAAAGCG 3606
QY 4331 GCCATTTCCACCATGATATTCGGCAAGCAGGATCCGCTGGCGTGGCGAGCCCTGTATG 4450
Db 3605 GCCATTTCCACCATGATATTCGGCAAGCAGGATCCGCTGGCGTGGCGAGCCCTGTATG 3486
QY 4391 GCGTGGGATGCGCGCTTGAGCCTTGGGAAACAGTTCGGCTGGCGGAGCCCTGTATG 4450
Db 3545 GCGTGGGATGCGCGCTTGAGCCTTGGGAAACAGTTCGGCTGGCGGAGCCCTGTATG 3486
QY 4451 CTCTCGTCAGATATCTGATGCGACAGACCGGCTTCATCCGAGTACGTCGCTC 4510
Db 3485 CTCTCGTCAGATATCTGATGCGACAGACCGGCTTCATCCGAGTACGTCGCTC 3426
QY 4511 GATCGATGTTTCGCTTGGTGGTTCGAATGGCAGGTAGCCGATCAAGCGTATGCGAGCG 4570
Db 3425 GATCGATGTTTCGCTTGGTGGTTCGAATGGCAGGTAGCCGATCAAGCGTATGCGAGCG 3366
QY 4571 CCGCATGTATCAGCATATGATGATATCTTCGCGAGGAGCAAGTGATGACAGGAG 4630
Db 3365 CCGCATGTATCAGCATATGATGATATCTTCGCGAGGAGCAAGTGATGACAGGAG 3306
QY 4631 ATCTGCCCCGACCTTCGCCAATAGCAGCAGTCCCTTCCGCTTCAGTACACAGTC 4690
Db 3305 ATCTGCCCCGACCTTCGCCAATAGCAGCAGTCCCTTCCGCTTCAGTACACAGTC 3246
QY 4691 GAGCAGCTGCGCAGGAAGACCGCCGCTGTCGCGAGCAGCAGTATGCGGCTGCTCGTC 4750
Db 3245 GAGCAGCTGCGCAGGAAGACCGCCGCTGTCGCGAGCAGCAGTATGCGGCTGCTCGTC 3186
QY 4751 CTGCAAGTTCAATCAGGCAACCGGACAGGTCCGTCTTGACAAAAGAACCGGCGCCCTG 4810
Db 3185 TTGCAAGTTCAATCAGGCAACCGGACAGGTCCGTCTTGACAAAAGAACCGGCGCCCTG 3126
QY 4811 CGCTCAGCGCGGAACACCGCGGATCAGAGCAGCGATGTCGTGTCGCCAGTCATA 4870
Db 3125 CGCTCAGCGCGGAACACCGCGGATCAGAGCAGCGATGTCGTGTCGCCAGTCATA 3066
QY 4871 GCCGAATAGCCTCTCCACCCAAAGCGCGGAGAACCTGGTGCAATTCATTGTTCAAT 4930
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Db 3065 GCCGAATAGCTCTCCACCAGAGCGCCGGAGAACTGCGTGAATCCATCTGTTCAAT 3006
QY 4931 CATGGAACGATCTCTCATCTCTGTCTTTGATCAGATCTTATCCCTCGGCATCAGAT 4990
Db 3095 CATGGAAACGATCTCTCATCTCTGTCTTTGATCAGAGCTTATCCCTCGGCATCAGAT 2946
QY 4991 CCTTCGCGGCAAGAAAGCATCCAGTTTACTTTTTCAGGGCTTCCCAACCTTACAGAGG 5050
Db 2945 CCTTCGCGGCAAGAAAGCATCCAGTTTACTTTTTCAGGGCTTCCCAACCTTACAGAGG 2886
QY 5051 CGCCCAAGCTGGCAATTCGGGTTCCGTTCTGTTGTCATATAAACCGCCAGCTAGCTATCG 5110
Db 2885 CGCCCAAGCTGGCAATTCGGGTTCCGTTCTGTTGTCATATAAACCGCCAGCTAGCTATCG 2826
QY 5111 CATGTAAAGCCACTGCAAGCTACTGCTTTCTTTTTCGCTTGGCTTTCCCTTGTCCA 5170
Db 2825 CATGTAAAGCCACTGCAAGCTACTGCTTTCTTTTTCGCTTGGCTTTCCCTTGTCCA 2766
QY 5171 GATAGCCAGTAGCTGACATTCATCCCGGGTCAGACCGTTTCTGCGACTGGTTTCTA 5230
Db 2765 GATAGCCAGTAGCTGACATTCATCCCGGGTCAGACCGTTTCTGCGACTGGTTTCTA 2706
QY 5231 CGTG 5234
Db 2705 CGTG 2702
```

## RESULT 6

US-10-021-403A-10

; Sequence 10, Application US/10021403A

; Publication No. US20030074679A1

; GENERAL INFORMATION:

; APPLICANT: Advysis

; TITLE OF INVENTION: Administration of Nucleic Acid Sequence to Female Animal to Enhanc

; FILE OF INVENTION: Growth in Offspring

; FILE REFERENCE: HO-P0201US/100021476/OTA 00-91

; CURRENT APPLICATION NUMBER: US/10/021,403A

; CURRENT FILING DATE: 2002-04-11

; PRIOR APPLICATION NUMBER: 60/255,021

; PRIOR FILING DATE: 2000-12-12

; NUMBER OF SEQ ID NOS: 11

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 10

; LENGTH: 2192

; TYPE: DNA

; ORGANISM: artificial sequence

; FEATURE:

; OTHER INFORMATION: This is a plasmid vector comprising a pVC0289 backbone

US-10-021-403A-10

## Query Match

Best Local Similarity 30.4%; Score 1603.8; DB 15; Length 2192;

Matches 2022; Conservative 0; Mismatches 27; Indels 392; Gaps 1;

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QY 2706 CTAGAGTAATCATGTCATAGCTGTTCTCTGTGGAATTTGTTATCCGCTCACAATTC 2765
Db 70 CTGGGTAAATCATGTCATAGCTGTTCTCTGTGGAATTTGTTATCCGCTCACAATTC 129
QY 2766 ACACAACATACGAGCCGGAAGCATAAAGTAAAGCTCGGGTGCCTAATGATGAGCTA 2825
Db 130 ACACAACATACGAGCCGGAAGCATAAAGTAAAGCTCGGGTGCCTAATGATGAGCTA 189
QY 2826 ACTCATTAAATTTGGTTCGCTCACTGCCGCTTTTCCAGTCGGGAAACCTTCGTCGCA 2885
Db 130 ACTCATTAAATTTGGTTCGCTCACTGCCGCTTTTCCAGTCGGGAAACCTTCGTCGCA 249
QY 2886 GCTGATTAAATGAATCGGCCAACCGCGGGAGAGCGGTTTGGCGGCTCTTC 2945
Db 250 GCTGATTAAATGAATCGGCCAACCGCGGGAGAGCGGTTTGGCGGCTCTTC 309
QY 2946 CGCTTCCTCGCTCACTGACTCGCTCGCTCGCTCGCTCGCTCGCTCGCTCGCTCGCT 3005
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[illegible]

QY	4086	GTATGGCAGGTTGGCGCTCGCTTGGTTCGATTTTCGAACCCACGAGTCCCGCTCAGAA	4145
Db	1108	-----GGCTCAGAAG	1117
QY	4146	AACTCGTCAGAAGCGCATAGAAGCGATGCGCTTGCGAATCGGAGCGCGGATACCGTAA	4205
Db	1118	AACTCGTCAGAAGCGCATAGAAGCGATGCGTTCGAATCGGAGCGCGGATACCGTAA	1177
QY	4206	AGCACGAGGAAGCGGTGAGCCATTGCGCGCGCAAGCTCTTCAGCAATATCACGGGTAGCC	4265
Db	1178	AGCACGAGGAAGCGGTGAGCCATTGCGCGCGCAAGCTCTTCAGCAATATCACGGGTAGCC	1237
QY	4266	AAACGCTATGCTCTGATAGCGGTTCGCGCACACCCAGCCGCGCACAGCTCGATGAATCCAGAA	4325
Db	1238	AAACGCTATGCTCTGATAGCGGTTCGCGCACACCCAGCCGCGCACAGCTCGATGAATCCAGAA	1297
QY	4326	AAGCGGCCATTTTCACCATGATATTCGGCAAGCAGGATTCGCCATGGTTCAGCAGGAGA	4385
Db	1298	AAGCGGCCATTTTCACCATGATATTCGGCAAGCAGGATTCGCCATGGTTCAGCAGGAGA	1357
QY	4386	TCCTCGCGGTGGGATACGCGCCTTGAGCTGGCGGAACAGTTTCGGCTTGGCGAGCGCC	4445
Db	1358	TCCTCGCGGTGGGATACGCGCCTTGAGCTGGCGGAACAGTTTCGGCTTGGCGAGCGCC	1417
QY	4446	TGATGCTCTTCGTCAGATCATCTCTGATCGACAAGACCGGCTTCATTCGAGTACGTGCT	4505
Db	1418	TGATGCTCTTCGTCAGATCATCTCTGATCGACAAGACCGGCTTCATTCGAGTACGTGCT	1477
QY	4506	CGCTCGATCGGATGTTTCGCTTGGTGGTTCGAATGGCAGGTACCGGATCAAGCGTATGC	4565
Db	1478	CGCTCGATCGGATGTTTCGCTTGGTGGTTCGAATGGCAGGTACCGGATCAAGCGTATGC	1537
QY	4566	AGCGCGCATTTGCATCAGCCATGATGATCTTTCTCGCAGGAGCAAGTGCAGTAC	4625
Db	1538	AGCGCGCATTTGCATCAGCCATGATGATCTTTCTCGCAGGAGCAAGTGCAGTAC	1597
QY	4626	AGGAGATCTGTCGCGGCACTTCGCCCAATAGCAGCAGTCCCTTCCCGCTTCAGTGACA	4685
Db	1598	AGGAGATCTGTCGCGGCACTTCGCCCAATAGCAGCAGTCCCTTCCCGCTTCAGTGACA	1657
QY	4686	AGTTCAGACAGCTCGCGAAGAAACGCCGCTCGTGGCCAGCCACGATAGCCGCTGCC	4745
Db	1658	AGTTCAGACAGCTCGCGAAGAAACGCCGCTCGTGGCCAGCCACGATAGCCGCTGCC	1717
QY	4746	TGCTCTCTGCAATTCATTACAGGACCGGACAGTTCGCTTTCGACAAAGAACCGGGCGC	4805
Db	1718	TGCTCTCTGCAATTCATTACAGGACCGGACAGTTCGCTTTCGACAAAGAACCGGGCGC	1777
QY	4806	CCCTGGCTGACAGCGGAAACAGCGCGGATTCAGAGCAGCGGATTCGTTGTCGCCAG	4865
Db	1778	CCCTGGCTGACAGCGGAAACAGCGCGGATTCAGAGCAGCGGATTCGTTGTCGCCAG	1837
QY	4866	TCCATAGCGGAATAGCTTCTCCACCAAGCGCGCGGAAACCTGCGTGCATTCATCTTGT	4925
Db	1838	TCCATAGCGGAATAGCTTCTCCACCAAGCGCGCGGAAACCTGCGTGCATTCATCTTGT	1897
QY	4926	TCAATATGCGAAACGATTCCTATCTCTGATCAGATCTTGATCCCTCGGCCAT	4985
Db	1898	TCAATATGCGAAACGATTCCTATCTCTGATCAGATCTTGATCCCTCGGCCAT	1957
QY	4986	CAGATCTTGGCGCAGAAAGCCATCCAGTTTACTTTGCAAGGCTTCCCAACCTTACCA	5045
Db	1958	CAGATCTTGGCGCAGAAAGCCATCCAGTTTACTTTGCAAGGCTTCCCAACCTTACCA	2017
QY	5046	GAGGCGCCCCAGCTGGCAATTCGGTTCGCTTCGATTAACACCGCCAGTCTAGC	5105
Db	2018	GAGGCGCCCCAGCTGGCAATTCGGTTCGCTTCGATTAACACCGCCAGTCTAGC	2077
QY	5106	TATGCCATGTAAAGCCACTCAAGCTACCTGCTTCTCTCT	5146
Db	2078	AACTGTTGGGAAGGCGCATTCGGTGGCGCTCTCTTCGCTATT	2118

RESULT 7  
US-10-359-919A-11  
; Sequence 11, Application US/10359919A  
; Publication No. US20040038918A1  
; GENERAL INFORMATION:  
; APPLICANT: Baylor College of Medicine  
; TITLE OF INVENTION: Modified Pituitary Gland Development in offspring from Explant  
; TITLE OF INVENTION: animals treated with GHRH  
; FILE REFERENCE: 109328.00087 - AVSI-0019  
; CURRENT APPLICATION NUMBER: US/10/359,919A  
; CURRENT FILING DATE: 2003-02-06  
; NUMBER OF SEQ ID NOS: 15  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 11  
; LENGTH: 3534  
; TYPE: DNA  
; ORGANISM: artificial sequence  
; FEATURE:  
; OTHER INFORMATION: Nucleic acid sequence of the HV-GHRH plasmid.  
US-10-359-919A-11

Query Match 30.4%; Score 1603.8; DB 13; Length 3534;  
Best Local Similarity 82.8%; Pred. No. 0;  
Matches 2022; Conservative 0; Mismatches 27; Indels 392; Gaps 1;  
QY 2706 CTAGACGTAATCATGTCATAGCTGTTCTCTGTGTGAATTTGTTATCGGTCACAATTC 2765  
DB 1412 CTTGGCGTAATCATGTCATAGCTGTTCTCTGTGTGAATTTGTTATCGGTCACAATTC 1471  
QY 2766 ACACAAATATGCGTTCGCTCACTGCGCGCTTCCTAGTCGGGAAACCTGTCGCCA 2885  
DB 1472 ACACAAATATGCGTTCGCTCACTGCGCGCTTCCTAGTCGGGAAACCTGTCGCCA 1591  
QY 2826 ACTCACATTAATGCGTTCGCTCACTGCGCGCTTCCTAGTCGGGAAACCTGTCGCCA 2885  
DB 1532 ACTCACATTAATGCGTTCGCTCACTGCGCGCTTCCTAGTCGGGAAACCTGTCGCCA 1591  
QY 2886 GCTGCATTAATGATCGGCCAAGCGCGGGAGAGCGGTTGCGTATTGGCGCTCTTC 2945  
DB 1592 GCTGCATTAATGATCGGCCAAGCGCGGGAGAGCGGTTGCGTATTGGCGCTCTTC 1651  
QY 2946 CGCTTCCTCGCTCACTGACTCGCTGCGCTGCGCTGCGCTGCGCTGCGCTGCGCTGCG 3005  
DB 1652 CGCTTCCTCGCTCACTGACTCGCTGCGCTGCGCTGCGCTGCGCTGCGCTGCGCTGCG 1711  
QY 3006 TCACTCAAGCGCGTAAATACGGTTATCCAGAAATCAGGGGATAACGAGGAAGAATCAT 3065  
DB 1712 TCACTCAAGCGCGTAAATACGGTTATCCAGAAATCAGGGGATAACGAGGAAGAATCAT 1771  
QY 3066 GTGAGCAAAAGCCAGCAAAAGCCAGCAACCGTAAGAGCGCGCTGCTGCGCTTTT 3125  
DB 1772 GTGAGCAAAAGCCAGCAAAAGCCAGCAACCGTAAGAGCGCGCTGCTGCGCTTTT 1831  
QY 3126 CCATAGGCTCCGCGCCCTGACGAGCATCACAAAATCAGCGCTCAAGTCAAGTGGG 3185  
DB 1832 CCATAGGCTCCGCGCCCTGACGAGCATCACAAAATCAGCGCTCAAGTCAAGTGGG 1891  
QY 3186 AAACCCGACGAGCTATAAGATACAGCGCTTCCCGCTGGAAGCTCCCTGTCGCTC 3245  
DB 1892 AAACCCGACGAGCTATAAGATACAGCGCTTCCCGCTGGAAGCTCCCTGTCGCTC 1951  
QY 3246 TCCGTTCGAGCTCCGCTTACCGGATACCTGTCGCGCTTTCCTTCGCGAAGCGT 3305  
DB 1952 TCCGTTCGAGCTCCGCTTACCGGATACCTGTCGCGCTTTCCTTCGCGAAGCGT 2011  
QY 3306 GCGCGCTTTCATAGCTCAGCTGTAGTATCTCAGTTCGGTGTAGTCTGCTCCAA 3365  
DB 2012 GCGCGCTTTCATAGCTCAGCTGTAGTATCTCAGTTCGGTGTAGTCTGCTCCAA 2071  
QY 3366 GCTGGGCTGTGACGAAACCCCGCTTCAGCCGACCGCTGCGCTTATCCGGTAACCTA 3425  
DB 2072 GCTGGGCTGTGACGAAACCCCGCTTCAGCCGACCGCTGCGCTTATCCGGTAACCTA 2131

QY 3426 TCGTCTTGAGTCCAAACCGGTAAAGACACGACTTATCGCCACTGGCAGCAGCACTGGTAA 3485  
DB 2132 TCGTCTTGAGTCCAAACCGGTAAAGACACGACTTATCGCCACTGGCAGCAGCACTGGTAA 2191  
QY 3486 CAGGATTAGCAGAGCGAGTATGAGCGGTCTACAGAGTCTTGAAGTGGTGGCTAA 3545  
DB 2192 CAGGATTAGCAGAGCGAGTATGAGCGGTCTACAGAGTCTTGAAGTGGTGGCTAA 2251  
QY 3546 CTACGGCTACACTAGAGAAACAGTATTTGGTATCTGCGCTCTGCTGAAGCCAGTTACCTT 3605  
DB 2252 CTACGGCTACACTAGAGAAACAGTATTTGGTATCTGCGCTCTGCTGAAGCCAGTTACCTT 2311  
QY 3606 CGGAAAAGAGTTGCTAGCTCTTGTATCCGGGAAACAAACCCAGCTGCTGAGCGGTGTT 3665  
DB 2312 CGGAAAAGAGTTGCTAGCTCTTGTATCCGGGAAACAAACCCAGCTGCTGAGCGGTGTT 2371  
QY 3666 TTTTGTTCGAAAGCAGCAGATTAACGCGCAGAAAAAGGATCTCAAGAGATCTCTTTGAT 3725  
DB 2372 TTTTGTTCGAAAGCAGCAGATTAACGCGCAGAAAAAGGATCTCAAGAGATCTCTTTGAT 2431  
QY 3726 CTTTCTACGGGCTGCTAGCTCAGCTCAGTGAACAAAACTCAGCTTAAAGGATTTTGGTCA 3785  
DB 2432 CTTTCTACGGGCTGCTGA----- 2449  
QY 3786 GAGATTATCGTCGACCAAGCGGCCATGTCCTCCCACTCTCTGAGTTCCGGGGCATG 3845  
DB 2450 ----- 2449  
QY 3846 GATGCGCGATGAGCGCTGCTGTTCTCTGATCCGACGATTTGCACTGCCGCTAGAA 3905  
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QY 3906 CTCGCGAGTCTGTCAGCTCAGCTCAGCAGCTGAACCACTCGCAGGGGATCGAGCC 3965  
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QY 3966 GGGGTGGCGAAGNACTCCAGCATGAGTCCCGCTGAGGATCATCCAGCGCGCTC 4025  
DB 2450 ----- 2449  
QY 4026 CCGGAAAAAGTTCGAAAGCCCAACTTTTCATAGAGCGCGCTGGAATCGAAATCTCG 4085  
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QY 4086 TGATGCGAGTTGGGCGTCTGTTGGTCTGTTTCGATTCGAAACCCAGAGTCCCGCTCA 4145  
DB 2450 -----CGCTCAGAG 2459  
QY 4146 AACTCGTCAAGAGCGATAGAGCGGATCGCTGCGATCGGAGCGGCGATACCGTAA 4205  
DB 2460 AACTCGTCAAGAGCGGATAGAGCGGATCGCTGCGATCGGAGCGGCGATACCGTAA 2519  
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DB 2520 AGCAGAGAGAGCGGTGAGCGGCTCAGCGGCTTCCGCGCAAGCTCTTCAAGATATCA 2579  
QY 4266 AACGCTATGCTCTGATGAGCGGCTCAGCGGCTCAGCGGCTCAGCGGCTCAGCGA 4325  
DB 2580 AACGCTATGCTCTGATGAGCGGCTCAGCGGCTCAGCGGCTCAGCGGCTCAGCGA 2639  
QY 4326 AAGCGGCTATTTCCACCATGATATTCGCAAGAGGATCGCCATGGGTCAAGCAGA 4385  
DB 2640 AAGCGGCTATTTCCACCATGATATTCGCAAGAGGATCGCCATGGGTCAAGCAGA 2699  
QY 4386 TCCTCGCGCTCGGCGATCGCGCTTGAAGCTTGAAGCTTGAAGCTTGAAGCTTGAAGCT 4445  
DB 2700 TCCTCGCGCTCGGCGATCGCGCTTGAAGCTTGAAGCTTGAAGCTTGAAGCTTGAAGCT 2759  
QY 4446 TGATGCTCTTCTGTCAGATCATCTCTGATCGAAGACCGGCTTCCATCCGAGTACGTCT 4505  
DB 2760 TGATGCTCTTCTGTCAGATCATCTCTGATCGAAGACCGGCTTCCATCCGAGTACGTCT 2819

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QY	2766	ACACAATACGAGCCGGAGCATAAAGATGTAAGCCCTGGGTGCCTAATAGTAGACTA	2825
DB	1472	ACACAATACGAGCCGGAGCATAAAGATGTAAGCCCTGGGTGCCTAATAGTAGACTA	1531
QY	2826	ACTCACATTAATCGGTTGGCTCATCTGCCGCTTCCAGTCGGGAAACCTGTCGTGCCA	2885
DB	1532	ACTCACATTAATCGGTTGGCTCATCTGCCGCTTCCAGTCGGGAAACCTGTCGTGCCA	1591
QY	2886	GCTGCATTAATCAATCGCCAAACGCGGGGAGAGCGGTTTCGCTATTGGCGCTCTTC	2945
DB	1592	GCTGCATTAATCAATCGCCAAACGCGGGGAGAGCGGTTTCGCTATTGGCGCTCTTC	1651
QY	2946	CGCTTCCTCGCTCACTGACTCGCTCGCTCGGTCGGTCGGCAGCGGTATCAGC	3005
DB	1652	CGCTTCCTCGCTCACTGACTCGCTCGCTCGGTCGGTCGGCAGCGGTATCAGC	1711
QY	3006	TCACTCAAAAGGCGTAATACGTTATCCACAGAAATCAGGGGATAAAGCAGGAAAGAACAT	3065
DB	1712	TCACTCAAAAGGCGTAATACGTTATCCACAGAAATCAGGGGATAAAGCAGGAAAGAACAT	1771
QY	3066	GTGAGCAAAAGGCCAGCAAAAGGCCAGGAACCGTTAAAGGCGCGTGTGCTGGCGTTTT	3125
DB	1772	GTGAGCAAAAGGCCAGCAAAAGGCCAGGAACCGTTAAAGGCGCGTGTGCTGGCGTTTT	1831
QY	3126	CCATAGGCTCGGCCCTTGACGAGCATCACAAAATTCGACGCTCAAGTCAGAGGTGGCG	3185
DB	1832	CCATAGGCTCGGCCCTTGACGAGCATCACAAAATTCGACGCTCAAGTCAGAGGTGGCG	1891
QY	3186	AAACCCGACAGGACTATAAGATACACAGGCGTTTCCCCCTGGAGCTCCCTCGTGGCGTC	3245
DB	1892	AAACCCGACAGGACTATAAGATACACAGGCGTTTCCCCCTGGAGCTCCCTCGTGGCGTC	1951
QY	3246	TCCGTGTCGACCCCTGCGCTTACCGGATACCTGTCGCGCTTCTCCCTTCGGGAAGCGT	3305
DB	1952	TCCGTGTCGACCCCTGCGCTTACCGGATACCTGTCGCGCTTCTCCCTTCGGGAAGCGT	2011
QY	3306	GGCGCTTCTCATAGCTACGCTGTAGGTATCTCAGTTCGGGTGATGGTTCGCTCCAA	3365
DB	2012	GGCGCTTCTCATAGCTACGCTGTAGGTATCTCAGTTCGGGTGATGGTTCGCTCCAA	2071
QY	3366	GCTGGGCTGTGCAAGAACCCCGCTTACGCCGACGCTGCGCTTATCGGTAACTA	3425
DB	2072	GCTGGGCTGTGCAAGAACCCCGCTTACGCCGACGCTGCGCTTATCGGTAACTA	2131

QY	3426	CTCGCTTTGAGTCCAAACCGGTAAGACACGACTTATCGCCACTGGCAGCAGCCACTGGTAA	2191
Db	2132	TCGCTTTGAGTCCAAACCGGTAAGACACGACTTATCGCCACTGGCAGCAGCCACTGGTAA	2191
QY	3486	CAGGATTAGCAGACGCGAGGTATGTAGGCGGTGCTACAGAGTCTTTGAAGTGGTGGCGCTAA	3545
Db	2192	CAGGATTAGCAGACGCGAGGTATGTAGGCGGTGCTACAGAGTCTTTGAAGTGGTGGCGCTAA	2251
QY	3546	CTACGGCTACACTAGAAGAACAGTATTTGGTGATCTGCGCTCTGCTGAAAGCCAGTTACCTT	3605
Db	2252	CTACGGCTACACTAGAAGAACAGTATTTGGTGATCTGCGCTCTGCTGAAAGCCAGTTACCTT	2311
QY	3606	CGGAAAAGAGTGTGTAGCTCTTGATCCGGCAAAACAAACCCGCTGGTAGCGGTGGTTT	3665
Db	2312	CGGAAAAGAGTGTGTAGCTCTTGATCCGGCAAAACAAACCCGCTGGTAGCGGTGGTTT	2371
QY	3666	TTTTGTTTGCAGCAGCAGATTACCGGCAGAAAAAAGGATCTCAAGAGATCCTTTGAT	3725
Db	2372	TTTTGTTTGCAGCAGCAGATTACCGGCAGAAAAAAGGATCTCAAGAGATCCTTTGAT	2431
QY	3726	CTTTTCTACGGGGTCTGACGCTCAGTGGNAACGAAAACTCACGTTAAGGATTTTGGTCAT	3785
Db	2432	CTTTTCTACGGGGTCTGACGCTCAGTGGNAACGAAAACTCACGTTAAGGATTTTGGTCAT	2449
QY	3786	GAGATTATCGTCGACCAAGCGGCCATCGTGCCTCCCACTCCTCGAGTTCGGGGGGCATG	3845
Db	2450	-----	2449

3846 GATGCGGATAGCCGCTGCTGGTTCTTGGATGCGGACGGATTGCACTGCGCGTAGAA 3905  
 2450 ----- 2449  
 3906 CTCGCGAGGTGTCACAGCTCAGGACGAGCTGAACCACTCGGAGGGATCGAGCC 3965  
 2450 ----- 2449  
 3966 GGGGTGGCGAAGAACTCAGCATGAGATCCCGCGCTGGAGGATCATCCAGCGCGCTC 4025  
 2450 ----- 2449  
 4026 CCGGAAACGATTCCGAAGCCCAACCTTTTCATAGAGGCGGGGTGGAATCGAAATCTCG 4085  
 2450 ----- 2449  
 4086 TGATGGCAGTTGGGCGTTCGCTTGGTGGTCAATTTGGAACCCAGAGTCCCGCTCAGAAG 4145  
 2450 ----- 2449  
 4146 AACTCGTCAAGAGCGGATAGAGCGGATGCTGGGAAATCGGAGCGCGATACCGGTAA 4205  
 2460 AACTCGTCAAGAGCGGATAGAGCGGATGCTGGGAAATCGGAGCGCGATACCGGTAA 2519  
 4206 AGCAGGAGGAGCGGTGAGCCATTGCGCGCAAGCTCTTCAGCAATATCAGGAGTACC 4265  
 2520 AGCAGGAGGAGCGGTGAGCCATTGCGCGCAAGCTCTTCAGCAATATCAGGAGTACC 2579  
 4266 AAGCTATGCTGATAGCGGTTCGCGCACACCCAGCGCGCACAGTTCGATGAATCCAGAA 4325  
 2580 AAGCTATGCTGATAGCGGTTCGCGCACACCCAGCGCGCACAGTTCGATGAATCCAGAA 2639  
 4326 AAGCGGCAATTTCCACCATGATATTCGGAAGAGGAGTCCCATCGGTACAGACGAGA 4385  
 2640 AAGCGGCAATTTCCACCATGATATTCGGAAGAGGAGTCCCATCGGTACAGACGAGA 2699  
 4386 TCCTCGCGCTCGGCGATCGCGCTTGAGCTTGGCGAACAGTTCGGTGGCGGAGCCCC 4445  
 2700 TCCTCGCGCTCGGCGATCGCGCTTGAGCTTGGCGAACAGTTCGGTGGCGGAGCCCC 2759  
 4446 TGATGCTCTTTCGTCAGATCATCTGATGACAAAGACCGGCTTCATCCGAGTACGTCG 4505  
 2760 TGATGCTCTTTCGTCAGATCATCTGATGACAAAGACCGGCTTCATCCGAGTACGTCG 2819  
 4506 CGCTCGATGCGATGTTTCGCTTGGTGGTTCGATGAGGAGGATGAGCGGTATGC 4565  
 2820 CGCTCGATGCGATGTTTCGCTTGGTGGTTCGATGAGGAGGATGAGCGGTATGC 2879  
 4566 AGCGCGCGATTCATCAGCATGATGATGATGATGATGATGATGATGATGATGATGATG 4625  
 2880 AGCGCGCGATTCATCAGCATGATGATGATGATGATGATGATGATGATGATGATGATG 2939  
 4626 AGGAGATCTGCGCGGCACTTCGCGCAATAGCAGCAGTCCCTTCGCGTTCAGTGACA 4685  
 2940 AGGAGATCTGCGCGGCACTTCGCGCAATAGCAGCAGTCCCTTCGCGTTCAGTGACA 2999  
 4686 AGCTCGAGCAGAGCTCGCAAGAACCGCGTGGTGGGAGGAGGAGGAGGAGGAGGAGGAG 4745  
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 4746 TCGTCTGAGTTCATTCAGGACCGGACAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 4805  
 3060 TCGTCTGAGTTCATTCAGGACCGGACAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 3119  
 4806 CCGTGGCTGACAGCGGAAACCGCGGATCAGAGCAGGCGGATTCGTTGTCGCGCAG 4865  
 3120 CCGTGGCTGACAGCGGAAACCGCGGATCAGAGCAGGCGGATTCGTTGTCGCGCAG 3179  
 4866 TCATAGCCGAATAGCTCTCCACCCAGCGGCGGAGAACCTGCGTGAATCCATCTTGT 4925  
 3180 TCATAGCCGAATAGCTCTCCACCCAGCGGCGGAGAACCTGCGTGAATCCATCTTGT 3239  
 4926 TCAATCATGCGAAACGATCT 4985

3240 TCAATCATGCGAAACGATCCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 3299  
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 3300 CAGATCCTTGGCGGCAAGAAAGCCATCCAGTTTATCTTTCAGGGCTTCCCAACCTTACCA 3359  
 5046 GAGGCGCGCCAGCTGCGCAATTCGGTTTCGTTGCTGCTGCTGCTGCTGCTGCTGCTGCT 5105  
 3360 GAGGCGCGCCAGCTGCGCAATTCGGTTTCGTTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3419  
 5106 TATCGCCATGTAAGCCCACTGCAAGCTACCTGCTTCTCTT 5146  
 3420 AACTGTTGGGAGGCGGATCGTGGGCGCTCTTCGCTATT 3460

RESULT 9

US-10-359-919A-13  
 ; Sequence 13, Application US/10359919A  
 ; Publication No. US20040038918A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Baylor College of Medicine  
 ; TITLE OF INVENTION: Modified Pituitary Gland Development in offspring from Expectant  
 ; FILE OF INVENTION: animals treated with GHRH  
 ; FILE REFERENCE: 108328.00087 - AVSI-0019  
 ; CURRENT APPLICATION NUMBER: US/10/359,919A  
 ; CURRENT FILING DATE: 2003-02-06  
 ; NUMBER OF SEQ ID NOS: 15  
 ; SOFTWARE: Patent in version 3.1  
 ; SEQ ID NO 13  
 ; LENGTH: 3534  
 ; TYPE: DNA  
 ; ORGANISM: artificial sequence  
 ; FEATURE:  
 ; OTHER INFORMATION: Nucleic acid sequence of the TV-GHRH plasmid.  
 US-10-359-919A-13

Query Match 30.4%; Score 1603.8; DB 13; Length 3534;  
 Best Local Similarity 82.8%; Pred. No. 0;  
 Matches 2022; Conservative 0; Mismatches 27; Indels 392; Gaps 1;  
 2706 CTAGACGTAATCATGCTCATGCTGTTTCTGCTGTGTAATTTATCCGCTCAAAATTC 2765  
 1412 CTGCGGTAATCATGCTCATGCTGTTTCTGCTGTGTAATTTATCCGCTCAAAATTC 1471  
 2766 ACACACATACGAGCGGAGGATTAAGTAAAGCTGGGTCCTTAATGAGTGAGCTA 2825  
 1472 ACACACATACGAGCGGAGGATTAAGTAAAGCTGGGTCCTTAATGAGTGAGCTA 1531  
 2826 ACTCACATTAATTGCGTTGCGTCACTGCGGCTTTCCAGTCGGGAAACCTGTCGTGCCA 2885  
 1532 ACTCACATTAATTGCGTTGCGTCACTGCGGCTTTCCAGTCGGGAAACCTGTCGTGCCA 1591  
 2886 GTGCAATTAATGAATCGGCAACCGCGCGGAGAGCGGTTTTCGTTGCGGCTCTTC 2945  
 1592 GCTGCATTAATGAATCGGCAACCGCGCGGAGAGCGGTTTTCGTTGCGGCTCTTC 1651  
 2946 CGCTTCCTGCTCACTGATCGCTGCGTTCGCTGCGTTCGCTGCGGCGGATATCAGC 3005  
 1652 CGCTTCCTGCTCACTGATCGCTGCGTTCGCTGCGTTCGCTGCGGCGGATATCAGC 1711  
 3006 TCACCTCAAGAGGGGTAATACGGTTATCCACAGAAATCAGGGGATACGAGGAAAGAAAT 3065  
 1712 TCACCTCAAGAGGGGTAATACGGTTATCCACAGAAATCAGGGGATACGAGGAAAGAAAT 1771  
 3066 GTGACAAAAGGCCAGCAAAAGGCCAGGAAACCGTAAAAAGGCGGTTCTGCTGCGCTTTT 3125  
 1772 GTGACAAAAGGCCAGCAAAAGGCCAGGAAACCGTAAAAAGGCGGTTCTGCTGCGCTTTT 1831  
 3126 CCATAGGCTTCGCGGCTTCGAGCATCAAAAAATCGAGCTCAAGTCAAGGTGAGGTCGG 3185  
 1832 CCATAGGCTTCGCGGCTTCGAGCATCAAAAAATCGAGCTCAAGTCAAGGTGAGGTCGG 1891





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; SEQ ID NO 14
; LENGTH: 3534
; TYPE: DNA
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: Nucleic acid sequence of the 15/27/28 GHRH plasmid.
US-10-359-919A-14

Query Match      30.4%; Score 1603.8; DB 13; Length 3534;
Best Local Similarity 82.8%; Pred. NO. 0;
Matches 2022; Conservative 0; Mismatches 27; Indels 392; Gaps 1;

QY 2706 CTAGACGTAATCATGGTCTATAGCTGTTTCCGTCGTGGAATGTTATCGCTCACAATTC 2765
|
Db 1412 CTTGGCGTAATCATGGTCTATAGCTGTTTCCGTCGTGGAATGTTATCGCTCACAATTC 1471
|
QY 2766 ACACAAATAGACGCGGGAACATAAAGTGTAAAGCCTTGGGTCGCTTAATGAGTGAGCTA 2825
|
Db 1472 ACACAAATAGACGCGGGAACATAAAGTGTAAAGCCTTGGGTCGCTTAATGAGTGAGCTA 1531
|
QY 2826 ACTCACATTAATTCGCTGCTCACTGCGCGCTTTCGAGTCGCGAAACCTTCGTGCCA 2885
|
Db 1532 ACTCACATTAATTCGCTGCTCACTGCGCGCTTTCGAGTCGCGAAACCTTCGTGCCA 1591
|
QY 2886 GCTGCATTAATGAATCGGCCAAACGCGGGGAGGCGGTTTSCGTATTGGCGCTCTTC 2945
|
Db 1592 GCTGCATTAATGAATCGGCCAAACGCGGGGAGGCGGTTTSCGTATTGGCGCTCTTC 1651
|
QY 2946 CGTTTCCTCGCTCACTGACTCGTTCGCTCGGTTCGTCGCTGCGGAGCGGTATCAGC 3005
|
Db 1652 CGTTTCCTCGCTCACTGACTCGTTCGCTCGGTTCGTCGCTGCGGAGCGGTATCAGC 1711
|
QY 3006 TCACCTAAAGCGGTAATACGGTTATCCACAGAAATCAGGGGTAACGACGAAAGACAT 3065
|
Db 1712 TCACCTAAAGCGGTAATACGGTTATCCACAGAAATCAGGGGTAACGACGAAAGACAT 1771
|
QY 3066 GTGAGCAAAAGGCCAGCAAAAGGCCAGGAAACCTGTAAGAGCGCGGTTTTCGCGTTT 3125
|
Db 1772 GTGAGCAAAAGGCCAGCAAAAGGCCAGGAAACCTGTAAGAGCGCGGTTTTCGCGTTT 1831
|
QY 3126 CCATAGGCTTCGCGCCCTCGACGAGCATCACAAAAATCGACGCTCAAGTCAGAGTGGG 3185
|
Db 1832 CCATAGGCTTCGCGCCCTCGACGAGCATCACAAAAATCGACGCTCAAGTCAGAGTGGG 1891
|
QY 3186 AAACCCGACAGACACTAATGAGTACAGGAGTTCGCCCTGGAAGTCCCTCGTGGCTC 3245
|
Db 1892 AAACCCGACAGACACTAATGAGTACAGGAGTTCGCCCTGGAAGTCCCTCGTGGCTC 1951
|
QY 3246 TCCTGTTCGACCCCTGCGCTTACCGGATACCTGTCCGCTTTCCTCCCTTCGCGAAGCGT 3305
|
Db 1952 TCCTGTTCGACCCCTGCGCTTACCGGATACCTGTCCGCTTTCCTCCCTTCGCGAAGCGT 2011
|
QY 3306 GCGCTTTCCTATAGTCAAGTGTAGTATCTCAGTTCGCTGAGTTCGCTTCCGCTCAA 3365
|
Db 2012 GCGCTTTCCTATAGTCAAGTGTAGTATCTCAGTTCGCTGAGTTCGCTTCCGCTCAA 2071
|
QY 3366 GCTGGCTGTGTCAGCAACCCCGTTTCAGCCGACCGCTGCGCTTATCCGTAACCTA 3425
|
Db 2072 GCTGGCTGTGTCAGCAACCCCGTTTCAGCCGACCGCTGCGCTTATCCGTAACCTA 2131
|
QY 3426 TCGTCTTGAGTCCAAACCCGTTAAGACACGACTTATCGCCACTGGCAGCGCACTGGTAA 3485
|
Db 2132 TCGTCTTGAGTCCAAACCCGTTAAGACACGACTTATCGCCACTGGCAGCGCACTGGTAA 2191
|
QY 3486 CAGGATTAGCAGAGCGAGTATGTAGGCGGTGCTACAGAGTTCCTTGAAGTGTGSCCTAA 3545
|
Db 2192 CAGGATTAGCAGAGCGAGTATGTAGGCGGTGCTACAGAGTTCCTTGAAGTGTGSCCTAA 2251
|
QY 3546 CTACGGCTACACTAGAAAGACAGTATTTGGTATCTGGCTCTGCTGGAAGCCAGTTACCTT 3605
|
Db 2252 CTACGGCTACACTAGAAAGACAGTATTTGGTATCTGGCTCTGCTGGAAGCCAGTTACCTT 2311
|
QY 3606 CGGAAAAAGAGTTGGTAGCTCTTGATCCGGCAAAACCAACCCGCTGCTAGCGGTGGTTT 3665
|
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Db 3240 TCAATCATGCGAAGCATCTCATCTCTCTTGATCAGATCTTGATCCCTCGGCCAT 3299  
QY 4986 CAGATCTCTGGCGGCAAGAAAGCCATCCAGTTTACTTTGACGGGCTTCCCAACCTTACCA 5045  
Db 3300 CAGATCTCTGGCGGCAAGAAAGCCATCCAGTTTACTTTGACGGGCTTCCCAACCTTACCA 3359  
QY 5046 GAGGCGCCCGAGTGGCAATTCGGTTCGCTGTGCTGCATTAAGCCGCGCTAGC 5105  
Db 3360 GAGGCGCCCGAGTGGCAATTCGGTTCGCTGTGCTGCATTAAGCCGCGCTAGC 3419  
QY 5106 TATGCCATGTAAGCCCACTCAAGCTACCTGCTTCTCTT 5146  
Db 3420 AACTGTTGGAGGCGATCGGTGCGGCCCTTCGCTATT 3460

RESULT 14  
US-10-315-907A-13  
; Sequence 13, Application US/10315907A  
; Publication No. US20040057941A1  
; GENERAL INFORMATION:  
; APPLICANT: Advisys  
; TITLE OF INVENTION: PLASMID MEDIATED SUPPLEMENTATION FOR TREATING CHRONICALLY ILL SUB  
; FILE REFERENCE: 108328.00073 - AVSI-0007  
; CURRENT APPLICATION NUMBER: US/10/315,907A  
; CURRENT FILING DATE: 2002-12-10  
; NUMBER OF SEQ ID NOS: 25  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 13  
; LENGTH: 3534  
; TYPE: DNA  
; ORGANISM: artificial sequence  
; FEATURE:  
; OTHER INFORMATION: Operatively linked components of the TV-GHRH plasmid.  
US-10-315-907A-13

Query Match 30.4%; Score 1603.8; DB 13; Length 3534;  
Best Local Similarity 82.8%; Pred. No. 0;  
Matches 2022; Conservative 0; Mismatches 27; Indels 392; Gaps 1;

QY 2706 CTAGAGCTAATCATGTCTAGTCTTTCTCTGTGTGAAATTTGTTATCCGCTCACAATTC 2765  
Db 1412 CTTGGGTAAATCATGTCTAGTCTTTCTCTGTGTGAAATTTGTTATCCGCTCACAATTC 1471  
QY 2766 ACAACAATACGAGCGGAGCAATAAGTGTAAAGCTGGGTGGCTTAATGATGAGCTA 2825  
Db 1472 ACAACAATACGAGCGGAGCAATAAGTGTAAAGCTGGGTGGCTTAATGATGAGCTA 1531  
QY 2826 ACTCACATTAATGCGTTGCGTCACTGCCCGCTTTCCAGTCGGGAAACCTGCTGCCA 2885  
Db 1532 ACTCACATTAATGCGTTGCGTCACTGCCCGCTTTCCAGTCGGGAAACCTGCTGCCA 1591  
QY 2886 GCTGCATTAATGAATCGGCCAAGCGCGGGAGAGCGGTTTGCATTTGGGCGCTCTTC 2945  
Db 1592 GCTGCATTAATGAATCGGCCAAGCGCGGGAGAGCGGTTTGCATTTGGGCGCTCTTC 1651  
QY 2946 CGTTCTCTCTCACTGACTCGTGTGCGTCACTGCCCGCTTTCCAGTCGGGAAACCTGCTGCCA 3005  
Db 1652 CGTTCTCTCTCACTGACTCGTGTGCGTCACTGCCCGCTTTCCAGTCGGGAAACCTGCTGCCA 1711  
QY 3006 TCACCTAAAGCGGTAAATACGGTTATCCACAGATCAGGGGATAACCGAGGAAAGACAT 3065  
Db 1712 TCACCTAAAGCGGTAAATACGGTTATCCACAGATCAGGGGATAACCGAGGAAAGACAT 1771  
QY 3066 GTGAGCAAAAGGCGCAAGAAAGCGGAGAACCGTAAAGCGCGTTGCTGGGTTTTT 3125  
Db 1772 GTGAGCAAAAGGCGCAAGAAAGCGGAGAACCGTAAAGCGCGTTGCTGGGTTTTT 1831  
QY 3126 CCATAGGCTCGGCCCTTACGAGCATCAAAAATCGAGCTCAAGTCAGAGTGGCG 3185  
Db 1832 CCATAGGCTCGGCCCTTACGAGCATCAAAAATCGAGCTCAAGTCAGAGTGGCG 1891  
QY 3186 AAACCCGACAGGACTATAAAGATACAGGCGTTTCCCGCTGGAAAGCTCCCTCGTGGCTC 3245

Db 1892 AAACCCGACAGGACTATAAGATACAGGCGTTTCCCGCTGGAAGCTCCCTCGTGGCGTC 1951  
QY 3246 TCCTGTTCCGACCTCGCGCTTACCGATACCTGTCCGCCCTTTCCTCCCTCGGGAAGCGT 3305  
Db 1952 TCCTGTTCCGACCTCGCGCTTACCGATACCTGTCCGCCCTTTCCTCCCTCGGGAAGCGT 2011  
QY 3306 GGCGCTTCTCATAGCTCACGCTGTAGGTATCTCAGTTTCGGTGTAGGTTCGTTCCGTCGA 3365  
Db 2012 GGCGCTTCTCATAGCTCACGCTGTAGGTATCTCAGTTTCGGTGTAGGTTCGTTCCGTCGA 2071  
QY 3366 GCTGGCTGTGTGACGAACCCCGCTTACCGCGACCGCTGCGCTTATCCGGTAACATA 3425  
Db 2072 GCTGGCTGTGTGACGAACCCCGCTTACCGCGACCGCTGCGCTTATCCGGTAACATA 2131  
QY 3426 TCCTGTTCCAGTCCCAACCCGCTAAGACAGACTTATCGCACTTTCGCGAGCAGCCACTGGTAA 3485  
Db 2132 TCCTGTTCCAGTCCCAACCCGCTAAGACAGACTTATCGCACTTTCGCGAGCAGCCACTGGTAA 2191  
QY 3486 CAGGATTAGCAGCGAGGTATGTAGCGGTGTCTACAGATTCTTGAAGTGTGGCCTAA 3545  
Db 2192 CAGGATTAGCAGCGAGGTATGTAGCGGTGTCTACAGATTCTTGAAGTGTGGCCTAA 2251  
QY 3546 CTACGGCTACACTAGAAAGACAGTATTTGGTATCTCGCTCTGCTGAAGCCAGTTACCTT 3605  
Db 2252 CTACGGCTACACTAGAAAGACAGTATTTGGTATCTCGCTCTGCTGAAGCCAGTTACCTT 2311  
QY 3606 CGGAAAAGAGTTGTTAGCTCTTGATCCGGCAAAACAAACCAACCGCTGTAGCGGTGTT 3665  
Db 2312 CGGAAAAGAGTTGTTAGCTCTTGATCCGGCAAAACAAACCAACCGCTGTAGCGGTGTT 2371  
QY 3666 TTTTGTTCGAAGCAGCAGATTACCGCGCAAAAAAAGATCTCAAGAGATCTTTGAT 3725  
Db 2372 TTTTGTTCGAAGCAGCAGATTACCGCGCAAAAAAAGATCTCAAGAGATCTTTGAT 2431  
QY 3726 CTTTCTACGGGTCTGAGCTCAGTGGAAACCAAACTCACGTTAAGGGATTGTTGTCAT 3785  
Db 2432 CTTTCTACGGGTCTGAG----- 2449  
QY 3786 GAGATTATCGTCGACCAAGCGGCATCGTGCCTCCACCTCCTGCAGTTTCGGGGGCGATG 3845  
Db 2450 ----- 2449  
QY 3846 GATGCGGATAGCCGCTGCTGTTCTGTGATGTCGCGAGGATTTGCATGCGCGTAGAA 3905  
Db 2450 ----- 2449  
QY 3906 CTCGCGAGGTGCTCAGCCTCAGGCAGCAGCTGAACCACTCGCGAGGGATCGAGCCC 3965  
Db 2450 ----- 2449  
QY 3966 GGGGTGGCGAAGAACTCCAGCATGAGATCCCGCGCTGGAGGATCATCCAGCGCGGCTC 4025  
Db 2450 ----- 2449  
QY 4026 CCGGAAAAACGATTCGAAAGCCAACTTTTCATGAAGGCGGCGTGAATCGAAATCTCG 4085  
Db 2450 ----- 2449  
QY 4086 TGATGGCAGTTGGGCGTCCGTTGGTCCGTCATTTTCGAACCCCGAGAGTCCCGCTCAGAAG 4145  
Db 2450 ----- 2459  
QY 4146 AACTCGTCAAGAAAGCGGATAGAAAGGCGATGCGTTCGAAATCGGAGCGGCGATACCGTAA 4205  
Db 2460 AACTCGTCAAGAAAGCGGATAGAAAGGCGATGCGTTCGAAATCGGAGCGGCGATACCGTAA 2519  
QY 4206 AGCAGGAGGAGCGGTGAGCCCATTCGCCCGCAGCTCTTTCAGCAATATCACGGGTAGCC 4265  
Db 2520 AGCAGGAGGAGCGGTGAGCCCATTCGCCCGCAGCTCTTTCAGCAATATCACGGGTAGCC 2579  
QY 4266 AACTGATGCTTATAGCGGTTCGCGCACACCCAGCGGCGCACAGTGCATGAATCCAGAA 4325  
Db 2580 AAGCGTATGCTCTGATAGCGGTTCGCGCACACCCAGCGGCGCACAGTGCATGAATCCAGAA 2639





QY	3666	TTTTTTTGAAGCAGCAGATTAACGCGCAGAAAAAAGGATCTCAGAAATCCTTTGAT	3725
Db	2372	TTTTTTTGAAGCAGCAGATTAACGCGCAGAAAAAAGGATCTCAGAAATCCTTTGAT	2431
QY	3726	CTTTTCTACGGGTCTGACGCTCAGTCAAGTCAAGGATTTTGGTCAAT	3785
Db	2432	CTTTTCTACGGGTCTGAT	2449
QY	3786	GAGATTATCGTCGACAAAGCGGCATCGTGCTCCCACTCCTGCAAGTTGCGGGGCATG	3845
Db	2450	-----	2449
QY	3846	GATCGCGGATAGCGCTGCTGTTTCTGGAGCCGACGGATTTGCACTGCCGGTAGAA	3905
Db	2450	-----	2449
QY	3906	CTCCCGAGGTGCTCCAGCCTCAGCAGCAGCTGAACCACTCGCGAGGGATGAGGCC	3965
Db	2450	-----	2449
QY	3966	GGGTGGGCGAAGAACTCCAGCATGAGATCCCGCGCTGGAGGATCATCCAGCCGGCGTC	4025
Db	2450	-----	2449
QY	4026	CCGGAAGCAATCCGAAGCCCAACCTTTCATAGAGGCGCGGTGGATCGAAATCTCG	4085
Db	2450	-----	2449
QY	4086	TGATGCGAGTTGGGCTGCTTGGTTCGTCATTTTCGAACCCAGAGTCCCGCTCAGAAG	4145
Db	2450	-----CGCTCAGAAG	2459
QY	4146	AACTCGTCAAGAGCGATAGAGGCGATGCGCTCGAATCGGAGCGCGGATACCGTAA	4205
Db	2460	AACTCGTCAAGAGCGATAGAGGCGATGCGCTCGAATCGGAGCGCGGATACCGTAA	2519
QY	4206	AGCAGAGAGGGTCAACCATTCGCGCCCAAGCTCTTCAGCAATATCAGGGTAGCC	4265
Db	2520	AGCAGAGAGGGTCAACCATTCGCGCCCAAGCTCTTCAGCAATATCAGGGTAGCC	2579
QY	4266	RACGCTATGCTGTAGAGGTCGCGCCACACCGCGCGCCACAGTTCGATGAATCCAGAA	4325
Db	2580	RACGCTATGCTGTAGAGGTCGCGCCACACCGCGCGCCACAGTTCGATGAATCCAGAA	2639
QY	4326	AAGCGGCCATTTTCCACCATGATATTCGGCAAGCAGGCTTCGCCATGGGTACGACGAGA	4385
Db	2640	AAGCGGCCATTTTCCACCATGATATTCGGCAAGCAGGCTTCGCCATGGGTACGACGAGA	2699
QY	4386	TCCTCGCGTGGGCGATGGCGCTTGAAGCTGGCGAAAGTTTCGGCTGGCGGAGCCCC	4445
Db	2700	TCCTCGCGTGGGCGATGGCGCTTGAAGCTGGCGAAAGTTTCGGCTGGCGGAGCCCC	2759
QY	4446	TGATGCTCTTCTGTCAGATCATCTGATCGAAGACCGGCTTCCATCCGAGTACGTGCT	4505
Db	2760	TGATGCTCTTCTGTCAGATCATCTGATCGAAGACCGGCTTCCATCCGAGTACGTGCT	2819
QY	4506	CGCTCGATGCGATGTTTCGCTTGGTGGTTCGAATGGGCGAGTACCGGATCAAGCGTATGC	4565
Db	2820	CGCTCGATGCGATGTTTCGCTTGGTGGTTCGAATGGGCGAGTACCGGATCAAGCGTATGC	2879
QY	4566	AGCGCGCGATTCGATCAGCATGATGATACCTTCTCGCAGGAGCAAGTGGATGAC	4625
Db	2880	AGCGCGCGATTCGATCAGCATGATGATACCTTCTCGCAGGAGCAAGTGGATGAC	2939
QY	4626	AGGAGATCTTCCCGGCACTTCGCCCAATAGCAGCCAGTCCCTTCCCGCTTCAGTGACA	4685
Db	2940	AGGAGATCTTCCCGGCACTTCGCCCAATAGCAGCCAGTCCCTTCCCGCTTCAGTGACA	2999
QY	4686	ACGTTCGAGCAGCTGCGCAGGAACCGCCGTCGTGGCCAGCCAGTACCGCGCTGCC	4745
Db	3000	ACGTTCGAGCAGCTGCGCAGGAACCGCCGTCGTGGCCAGCCAGTACCGCGCTGCC	3059
QY	4746	TCGTCCTCGAGTTTCAATTCAGGGCAGCGGATCGGTCTTGACAAAAAGAACCGGGCGC	4805

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Job time : 2268 secs

GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: August 4, 2004, 04:18:02 ; Search time 12184 Seconds

(without alignments)

12948.285 Million cell updates/sec

Title: US-09-921-143-36

Perfect score: 5283

Sequence: 1 aagcttgacctatgcgact.....tgagtgcttgcgcgagcgtg 5283

Scoring table: IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0

Searched: 27513289 seqs, 14931090276 residues

Total number of hits satisfying chosen parameters: 55026578

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: em\_estba:\*

2: em\_esthum:\*

3: em\_estin:\*

4: em\_estmu:\*

5: em\_estov:\*

6: em\_estpl:\*

7: em\_estro:\*

8: em\_estc:\*

9: gb\_estl:\*

10: gb\_est2:\*

11: gb\_estc:\*

12: gb\_est3:\*

13: gb\_est4:\*

14: gb\_est5:\*

15: em\_estfun:\*

16: em\_estom:\*

17: em\_gss\_hum:\*

18: em\_gss\_inv:\*

19: em\_gss\_pln:\*

20: em\_gss\_vrt:\*

21: em\_gss\_fun:\*

22: em\_gss\_mam:\*

23: em\_gss\_mus:\*

24: em\_gss\_pro:\*

25: em\_gss\_rod:\*

26: em\_gss\_pbg:\*

27: em\_gss\_vrl:\*

28: gb\_gssl:\*

29: gb\_gss2:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	991	18.8	2450	11	AK047844
2	948	17.9	1067	9	AU081137
C 3	939.4	17.8	954	14	CK283361
C 4	924.6	17.5	947	14	CK298208

5	919.8	17.4	1089	9	AU081124
C 6	918.6	17.4	935	14	CK284786
C 7	911	17.2	936	14	CK256977
C 8	907	17.2	910	14	CK287930
9	899.6	17.0	1025	29	CG700598
10	898.8	17.0	996	29	CG392995
C 11	886.4	16.8	933	14	CK291799
C 12	883.6	16.7	1021	29	CG392916
C 13	875	16.6	925	14	CB686151
14	866.2	16.4	1073	14	CF269652
15	849	16.1	1056	29	CG835880
C 16	843	16.0	856	14	CK287297
17	814.4	15.4	906	29	CG839154
18	809.2	15.3	966	28	BZ570738
C 19	803	15.2	804	14	CK291519
C 20	794	15.0	811	14	CK288185
21	781.2	14.8	1163	9	AU081044
22	781.2	14.8	1249	28	BZ572284
23	780.8	14.8	831	12	BG680919
24	780.8	14.8	858	14	CA488579
C 25	780.6	14.8	833	14	CB686421
26	774	14.7	954	9	AL044364
27	769.2	14.6	863	14	CF752100
C 28	760.8	14.4	878	14	CK288711
29	754	14.3	1369	28	BZ579291
30	746	14.1	844	28	BZ574513
31	742.2	14.0	1346	28	BZ572730
32	740.8	14.0	914	28	BZ569398
33	740.4	14.0	831	29	TBR548748
34	740	14.0	1194	28	BZ578985
C 35	734.8	13.9	811	29	ATH517156
36	725.6	13.7	959	28	BZ557985
37	719.6	13.6	847	28	AZ687169
38	719.6	13.6	854	28	BZ570648
39	719.4	13.6	896	28	BZ551301
40	718.4	13.6	800	9	AJ281449
41	711	13.5	1004	9	AJ281480
42	708	13.4	828	28	BZ573391
43	707.6	13.4	835	28	BZ571572
44	704	13.3	818	12	B1180988
45	700.2	13.3	838	28	AZ679307

## ALIGNMENTS

RESULT 1  
AK047844

LOCUS

DEFINITION

AK047844 2450 bp mRNA linear HTC 20-SEP-2003  
Mus musculus 16 days embryo head cDNA, RIKEN full-length enriched  
library, clone:Cl30004M09 product:vascular endothelial growth  
factor C, full insert sequence.

ACCESSION

VERSION AK047844.1 GI:26339001

KEYWORDS

SOURCE HTC; CAP trapper.

ORGANISM

Mus musculus (house mouse)

REFERENCE

AUTHORS

TITLE High-efficiency full-length cDNA cloning

JOURNAL Meth. Enzymol. 303, 19-44 (1999)

MEDLINE 99279253

PUBMED 10349636

REFERENCE

AUTHORS

TITLE

JOURNAL

MEDLINE

PUBMED

AK047844 2450 bp mRNA linear HTC 20-SEP-2003  
Mus musculus 16 days embryo head cDNA, RIKEN full-length enriched  
library, clone:Cl30004M09 product:vascular endothelial growth  
factor C, full insert sequence.

AK047844  
Mus musculus  
HTC; CAP trapper.  
Mus musculus (house mouse)  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
1  
Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K.,  
Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.  
Normalization and subtraction of cap-trapper-selected cDNAs to  
prepare full-length cDNA libraries for rapid discovery of new genes  
Genome Res. 10 (10), 1617-1630 (2000)  
20499374  
PUBMED 11042159







callus tissue and root tissue"  
/lab\_host="DH10B-TorA"  
/clone\_lib="Nicotiana benthamiana mixed tissue cDNA  
library, normalized, full-length"  
/notes="Vector: pCMVSPORT6.1; Site1: EcoRI; Site 2: NotI;  
supplier: RNA was isolated from Nicotiana benthamiana  
tissues that include callus, roots from liquid culture  
grown plants, heat-stressed leaves (38 C, 3 hr and 6 hr),  
cold-stressed leaves (5 C 3 hr, 6hr), and pathogen  
challenged leaves (Pseudomonas syringae pv tomato 12 hr;  
Xanthomonas campestris pv campestris 12 hr, 18hr;  
Pseudomonas syringae pv phaseolicola 18hr, and Xanthomonas  
campestris pv vesicatoria 16hr). RNA was isolated from  
these tissues and pooled in approximately equal molar  
amounts."

## ORIGIN

Query Match	17.5%	Score	924.6	DB	14	Length	947
Best Local Similarity	99.6%	Pred. No.	8.7e-215				
Matches	927	Conservative	0	Mismatches	4	Indels	0
						Gaps	0
QY	4001	GCTGGAGGATCATCCACGCGGCTCCGGAAACGATTCCGAAGCCCAACTTTCATAGA	4060				
Db	947	GCTGGAGGATCATCCACGCGGCTCCGGAAACGATTCCGAAGCCCAACTTTCATAGA	888				
QY	4061	AGCGCGCGGTGGAATCGAAATCTCGTGATGGCAGGTTGGCGTCGCTTCGTCGGTCATTT	4120				
Db	887	AGCGCGCGGTGGAATCGAAATCTCGTGATGGCAGGTTGGCGTCGCTTCGTCGGTCATTT	828				
QY	4121	CGAAACCCAGAGTCCCGCTCAGAAAGAACTCGTCAAGAGCGGATAGAGCGATGCGCTG	4180				
Db	827	CGAAACCCAGAGTCCCGCTCAGAAAGAACTCGTCAAGAGCGGATAGAGCGATGCGCTG	768				
QY	4181	CGAATCGGAGCGGGGATACCGTAAAGACAGAGGAAGCGGTAGCCCATTCGCGCGCAAG	4240				
Db	767	CGAATCGGAGCGGGGATACCGTAAAGACAGAGGAAGCGGTAGCCCATTCGCGCGCAAG	708				
QY	4241	CTCTTCAGCAATATCAACGGGTAGCCAAACGCTATGTCTGATAGCGGTCCGCCACACCCAG	4300				
Db	707	CTCTTCAGCAATATCAACGGGTAGCCAAACGCTATGTCTGATAGCGGTCCGCCACACCCAG	648				
QY	4301	CCGGCCACAGTCGATGAATCCAGAAAGCGGCATTTCCACATGATATTCGGAAGCA	4360				
Db	647	CCGGCCACAGTCGATGAATCCAGAAAGCGGCATTTCCACATGATATTCGGAAGCA	588				
QY	4361	GGCATCGCAATGGGTCAACAGAGATCCTCGCGCTCGGSCATCGCGCTTCAGCGCTGC	4420				
Db	587	GGCATCGCAATGGGTCAACAGAGATCCTCGCGCTCGGSCATCGCGCTTCAGCGCTGC	528				
QY	4421	GAAACAGTTTCGGTGGCGGAGCCCTGATGCTCTTCGTCAGATCATCTCTGATCGACAAG	4480				
Db	527	GAAACAGTTTCGGTGGCGGAGCCCTGATGCTCTTCGTCAGATCATCTCTGATCGACAAG	468				
QY	4481	ACCGCTTCCATCCGAGTACGTGCTCGTTCGATGCGATGTTTCGTTGCTGTCGAATGG	4540				
Db	467	ACCGCTTCCATCCGAGTACGTGCTCGTTCGATGCGATGTTTCGTTGCTGTCGAATGG	408				
QY	4541	GCAGTAGCCGGATCAAGGATATGAGCGCCGCGAATGCATCAGCCATGATGGATACTTT	4600				
Db	407	GCAGTAGCCGGATCAAGGATATGAGCGCCGCGAATGCATCAGCCATGATGGATACTTT	348				
QY	4601	CTCGCAGGACGAAGGTGAGATGACAGAGATCCTGCCCGGCACTTCGCCCAATAGCAG	4660				
Db	347	CTCGCAGGACGAAGGTGAGATGACAGAGATCCTGCCCGGCACTTCGCCCAATAGCAG	288				
QY	4661	CCAGTCCCTTCCCGTTCAGTGACAACTCGAGCAAGCTCGCAAGGAAAGCCCGTCGT	4720				
Db	287	CCAGTCCCTTCCCGTTCAGTGACAACTCGAGCAAGCTCGCAAGGAAAGCCCGTCGT	228				
QY	4721	GGCCAGCCACGATAGCCGGTGCCTCGTCTGAGTTCAITTCAGGGCACCGGACAGGTC	4780				
Db	227	GGCCAGCCACGATAGCCGGTGCCTCGTCTGAGTTCAITTCAGGGCACCGGACAGGTC	168				

QY	4781	GGTCTTGACAAAAGAACCGGGGCCCTCGCTGACAGCCGGAACACGGCGCATCAGA	4844
Db	167	GGTCTTGACAAAAGAACCGGGGCCCTCGCTGACAGCCGGAACACGGCGCATCAGA	108
QY	4841	GCAGCCGATGTCTGTGTGTCGCCAGTCATAGCCGATAGCCTCTCCACC	4900
Db	107	GCAGCCGATGTCTGTGTGTCGCCAGTCATAGCCGATAGCCTCTCCACC	48
QY	4901	AGAACCTGCGTGAATCCATCTTTGTTCAATC	4931
Db	47	AGAACCTGCGTGAATCCATCTTTGTTCAATC	17
RESULT 5			
LOCUS	AU081124	1089 bp	linear
DEFINITION	AU081124	Oncorhynchus mykiss Kidney infected by infectious hematopoietic necrosis virus	EST 30-JUL-2002
ACCESSION	AU081124		
VERSION	AU081124		
KEYWORDS	AU081124.1	GI:6431472	
SOURCE	Oncorhynchus mykiss	(rainbow trout)	
ORGANISM	Oncorhynchus mykiss		
REFERENCE			
AUTHORS	Kono,T., Sakai,M. and Lapatra,S.E.		
TITLE	Expressed Sequence Tag Analysis of Kidney and Gill Tissues from Rainbow Trout (Oncorhynchus mykiss) Infected with Infectious Hematopoietic Necrosis Virus		
JOURNAL	Mar. Biotechnol. 2 (5), 493-498 (2001)		
COMMENT	Contact: Masahiro Sakai Faculty of Agriculture Miyazaki University 1-1 nishi gakuenikibanadai, Miyazaki, Miyazaki 889-2192, Japan Email: m.sakai@cc.miyazaki-u.ac.jp.		
FEATURES			
source	1. 1089 /organism="Oncorhynchus mykiss" /mol_type="mRNA" /db_xref="taxon:8022" /clone="KG'12" /tissue_type="kidney" /clone_lib="Oncorhynchus mykiss Kidney infected by infectious hematopoietic necrosis virus" /note="common name:rainbow trout ; infected by infectious hematopoietic necrosis virus"		
ORIGIN			
Query Match	17.4% ;	Score 919.8 ;	DB 9 ;
Best Local Similarity	97.2% ;	Pred. No. 1.4e-213 ;	Length 1089 ;
Matches	979 ;	Conservative 0 ;	Mismatches 22 ;
			Indels 6 ;
			Gaps 4 ;
QY	2706	CTAGACGTAATCATGGTCATAGCTGTTTCCTGTGTGAATTTGTTATCCGTCACAAATTC	2765
Db	83	CTTGGCGTAATCATGGTCATAGCTGTTTCCTGTGTGAATTTGTTATCCGTCACAAATTC	142
QY	2766	ACACAACATACAGCGCGGAAGCATAAAGTGTAAAGCCTGGGGTGCCTAATGAGTGAGCTA	2825
Db	143	ACACAACATACAGCGCGGAAGCATAAAGTGTAAAGCCTGGGGTGCCTAATGAGTGAGCTA	202
QY	2826	ACTCACATTAATTCGGTTCGGCTCACTGCCGCTTTCAGTCGGGAAACCTGTGTCGCCA	2885
Db	203	ACTCACATTAATTCGGTTCGGCTCACTGCCGCTTTCAGTCGGGAAACCTGTGTCGCCA	262
QY	2886	GCTGCATTAAATGAATCGGCCAACCGCGGGGAGAGCGGTTTGGTATTCGGCGCTCTTC	2945
Db	263	GCTGCATTAAATGAATCGGCCAACCGCGGGGAGAGCGGTTTGGTATTCGGCGCTCTTC	322
QY	2946	CGTTCTTCGCTCACTGACTCGCTCGGCTCGGTCGGTTCGGTTCGGTCGGCGAGCGSTATCAGC	3005





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Db      335  |||||GATCTGCCCCGACCTTCCGCCCAATAGCAGCGAGTCCCTTCCCGCTTCAGTGCAACGCT 276
QY      4690  CGAGCACAGCTCCGCAAGAAACCCCGTCTGTCGCGCAGCCACGATAGCCGCGTCTGCTCGT 4749
Db      275  CGAGCACAGCTCCGCAAGAAACCCCGTCTGTCGCGCAGCCACGATAGCCGCGTCTGCTCGT 216
QY      4750  CCTGCAGTTCATTCAGGGACCCGACAGCTCGGTCTTGACAAAGAAACCCGCGCCCT 4809
Db      215  CCTGCAGTTCATTCAGGGACCCGACAGCTCGGTCTTGACAAAGAAACCCGCGCCCT 156
QY      4810  GCGCTGACAGCCGGAACACGCGGCGATCAGAGCAGCGATTCCTGTTGCGCCAGTCA 4869
Db      155  GCGCTGACAGCCGGAACACGCGGCGATCAGAGCAGCGATTCCTGTTGCGCCAGTCA 96
QY      4870  AGCCGAATAGCTCTCCACCCAGCGCGGAGAACCTGCGTGCATCCATCTTGTCAA 4929
Db      95  AGCCGAATAGCTCTCCACCCAGCGCGGAGAACCTGCGTGCATCCATCTTGTCAA 36
QY      4930  TCATGCGAAAGCATCTCATCTGT 4954
Db      35  TCAITCGAAACGATCCAGATCCGGT 11

RESULT 7
LOCUS   CK256977/c
DEFINITION EST740614 potato callus cDNA library, linear EST 12-DEC-2003
Solanum tuberosum cDNA clone POCD170 5' end, mRNA sequence.
ACCESSION CK256977
VERSION   CK256977.1 GI:39813957
KEYWORDS EST.
SOURCE   Solanum tuberosum (potato)
ORGANISM Solanum tuberosum
REFERENCE
AUTHORS  Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
TITLE     Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
JOURNAL   asterids; lamids; Solanales; Solanaceae; Solanum.
COMMENT   1 (bases 1 to 936)
Buell,C.R., Hart,A., Zismann,V., Karamycheva,S.A. and Baker,B.
Generation of ESTs from potato callus tissue
Unpublished (2003)
Contact: Robin Buell
The Institute for Genomic Research
9712 Medical Center Dr, Rockville, MD 20850, USA
Email: potato-array@tigr.org
Clones can be requested from TIGR via potato@tigr.org
Seq primer: ATT TAG GTG ACA CTA TAG.
FEATURES
source   1..936
          /organism="Solanum tuberosum"
          /mol_type="mRNA"
          /cultivar="Kennebec"
          /db_xref="taxon:4113"
          /clone="POCD170"
          /tissue_type="callus"
          /lab_host="DH10B-Tona"
          /clone_lib="potato callus cDNA library, normalized and
          full-length"
          /notes="Vector: pCMVSPORT6.1; Site 1: EcoRI; Site 2: NotI;
          supplier: RNA was isolated from Solanum tuberosum var.
          Kennebec callus tissue grown on solid media."

ORIGIN
Query Match 17.2%; Score 911; DB 14; Length 936;
Best Local Similarity 99.9%; Pred. No. 1.9e-211;
Matches 922; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY      4010  TCATCCAGCGCGGTGCC-GGAAACGATTCCGAAGCCCAACCTTTTCATAGAAGCGGCG 4068
Db      936  TCATCCAGCGCGGTCCCGGAAACGATTCCGAAGCCCAACCTTTTCATAGAAGCGGCG 877
QY      4069  GTGGAATCGAAATCTCGTGTATGTCAGGTTGGGCGTTCGTTGTCGGTCAATTCGAACCCC 4128

```

RESULT 8  
 CK287930/c  
 LOCUS  
 DEFINITION  
 CK287930  
 EST750652 Nicotiana benthamiana mixed tissue cDNA library,  
 normalized, full-length Nicotiana benthamiana cDNA clone NBMC75 5'  
 end, mRNA sequence.  
 CK287930.1 GI:39864940  
 ACCESSION  
 VERSION  
 KEYWORDS  
 SOURCE  
 ORGANISM

910 bp mRNA linear EST 15-DEC-2003  
 EST750652 Nicotiana benthamiana mixed tissue cDNA library,  
 normalized, full-length Nicotiana benthamiana cDNA clone NBMC75 5'  
 end, mRNA sequence.  
 CK287930  
 EST.  
 Nicotiana benthamiana  
 Nicotiana benthamiana  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
 asterids; lamids; Solanales; Solanaceae; Nicotiana.

REFERENCE 1 (bases 1 to 910)  
AUTHORS Buell, C.R., Hart, A., Zismann, V., Karamycheva, S.A., Day, B.,  
Staskawicz, B., Jin, H., and Baker, B.  
TITLE Generation of EST sequences from Nicotiana benthamiana  
JOURNAL Unpublished (2003)  
COMMENT Other ESTs: EST750653  
Contact: Robin Buell  
The Institute for Genomic Research  
9712 Medical Center Dr, Rockville, MD 20850, USA  
Email: potato-array@tigr.org  
Clones can be requested from TIGR via potato@tigr.org  
Seq primer: ANT TAG GTG ACA CTA TAG.  
Location/Qualifiers  
1. .910  
/organism="Nicotiana benthamiana"  
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/db\_xref="taxon:4100"  
/clone="NBMBC75"  
/tissue\_type="abiotic and biotic stress-treated leaves,  
callus tissue and root tissue"  
/lab\_host="DH10B-Tona"  
/clone\_lib="Nicotiana benthamiana mixed tissue cDNA  
library, normalized, full-length"  
/note="Vector: pCMVSPORT6.1; Site 1: EcoRI; Site 2: NotI;  
supplier: RNA was isolated from Nicotiana benthamiana  
tissues that include callus, roots from liquid culture  
grown plants, heat-stressed leaves (38 C, 3 hr and 6 hr),  
cold-stressed leaves (5 C 3 hr, 6hr), and pathogen  
challenged leaves (Pseudomonas syringae pv tomato 12 hr;  
Xanthomonas campestris pv campestris 12 hr, 16hr;  
Pseudomonas syringae pv phaseolicola 18hr, and Xanthomonas  
campestris pv vesicatoria 18hr). RNA was isolated from  
these tissues and pooled in approximately equal molar  
amounts."

ORIGIN  
Query Match 17.2%; Score 907; DB 14; Length 910;  
Best Local Similarity 100.0%; Pred. No. 1.7e-210; Indels 0; Gaps 0;  
Matches 907; Conservative 0; Mismatches 0

QY 4025 CCGGAAACGATTCGGAAGCCCAACCTTTTCATAGAGGGCGGTGGAATCGAATCTC 4084  
DB 910 CCGGAAACGATTCGGAAGCCCAACCTTTTCATAGAGGGCGGTGGAATCGAATCTC 851  
QY 4085 GTGATGCAGGTGGGCGTCTTGGTGGTTCATTTGAAACCCAGAGTCCCGTCA 4144  
DB 850 GTGATGCAGGTGGGCGTCTTGGTGGTTCATTTGAAACCCAGAGTCCCGTCA 791  
QY 4145 GAACCTCTCAAGAGCGATAGAGGGGATCGCTGCGAATCGGGCGGATACCGTA 4204  
DB 790 GAACCTCTCAAGAGCGGATAGAGGGGATCGCTGCGAATCGGGCGGATACCGTA 731  
QY 4205 AAGCAGGAGGAGGCGTCAAGCCCATTCGCCGCCAAGCTTTTCAGCAATATCACGGTAGC 4264  
DB 730 AAGCAGGAGGAGGCGTCAAGCCCATTCGCCGCCAAGCTTTTCAGCAATATCACGGTAGC 671  
QY 4265 CAACGCTATGTCGTATAGCGGTTCGCCACACCCAGCGGCCACAGTCATCCAGA 4324  
DB 670 CAACGCTATGTCGTATAGCGGTTCGCCACACCCAGCGGCCACAGTCATCCAGA 611  
QY 4325 AAAGCGGCATTTCCACCATGATATTTCGGAAGCAGGATCGCCATGGGTCAAGCAG 4384  
DB 610 AAAGCGGCATTTCCACCATGATATTTCGGAAGCAGGATCGCCATGGGTCAAGCAG 551  
QY 4385 ATCCTCGCGGTTCGGGATCGCGCTTCAGCTTCGCAACAGTTTCGGTTCGGCGGAGCCC 4444  
DB 550 ATCCTCGCGGTTCGGGATCGCGCTTCAGCTTCGCAACAGTTTCGGTTCGGCGGAGCCC 491  
QY 4445 CTGATGCTCTTCGTCCAGATCATCTCTGATCGACAGCGGCTTCATCCGAGTACGCGC 4504  
DB 490 CTGATGCTCTTCGTCCAGATCATCTCTGATCGACAGCGGCTTCATCCGAGTACGCGC 431  
QY 4505 TCGCTCGATGCGATGTTTTCGCTTGGTGGTTCGGAATGGGCGAGGTAGCCGGATCAAGCGTATG 4564

Db 430 TCGCTCGATCGATGTTTCGCTTGGTGGTTCGAATGGCAGGTAGCGCGATCAAGCGTAG 371  
QY 4565 CAGCGCGCGCATTCGATCAGCCATGATGATATCTTCTCGGAGGAGCAAGTGAATGA 4624  
Db 370 CAGCGCGCGCATTCGATCAGCCATGATGATATCTTCTCGGAGGAGCAAGTGAATGA 311  
QY 4625 CAGGAGATCCTGCGCGGCACTTCGCCCAATAGCAGCCAGTCCCTTCCGCTTCAGTGAC 4684  
Db 310 CAGGAGATCCTGCGCGGCACTTCGCCCAATAGCAGCCAGTCCCTTCCGCTTCAGTGAC 251  
QY 4685 AACGTCGAGCAGCAGTTCGCGCAAGAGCGCGCTCGTGGCCAGCAGATAGCGCGCTGC 4744  
Db 250 AACGTCGAGCAGCAGTTCGCGCAAGAGCGCGCTCGTGGCCAGCAGATAGCGCGCTGC 191  
QY 4745 CTGCTCCTCAGTTCATTCAGGCGCACCGGACAGGTGCGTCTTGACAAAAGAACCGGGCG 4804  
Db 190 CTGCTCCTCAGTTCATTCAGGCGCACCGGACAGGTGCGTCTTGACAAAAGAACCGGGCG 131  
QY 4805 CCGCTCGCTGAGCAGCGCGGAACACCGCGGCATCAGAGCGCGGATTCGTGTGTCGCCA 4864  
Db 130 CCGCTCGCTGAGCAGCGCGGAACACCGCGGCATCAGAGCGCGGATTCGTGTGTCGCCA 71  
QY 4865 GTCATAGCGAATAGCTCTCCACCCAGCGCGGAGACCTGCGTGAATCCATCTTG 4924  
Db 70 GTCATAGCGAATAGCTCTCCACCCAGCGCGGAGAACCTGCGTGAATCCATCTTG 11  
QY 4925 TTCAATC 4931  
Db 10 TTCAATC 4

RESULT 9  
CG700598  
LOCUS ZMMBHC0120G04f ZMMBHC (EcoRI) Zea mays subsp. mays genomic clone  
DEFINITION ZMMBHC0120G04 5', genomic survey sequence.  
ACCESSION CG700598  
VERSION CG700598.1 GI:37688399  
KEYWORDS GSS.  
SOURCE Zea mays subsp. mays (maize)  
ORGANISM Zea mays subsp. mays  
Ze mays subsp. mays  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACAD  
clade; Panicoideae; Andropogoneae; Zea.  
REFERENCE 1 (bases 1 to 1025)  
AUTHORS Bharti, A.K., Young, S., Kavchok, S., Keizer, G., Bronzino, A.C.,  
Zohovetz, I., Fuks, G., Yu, Y., Wing, R., and Messing, J.  
TITLE Sequencing of the maize genome at FGI (2003c)  
JOURNAL Unpublished (2003)  
COMMENT Contact: Bharti, A.K.  
Dr. Joachim Messing's lab  
The Plant Genome Initiative at Rutgers, Waksman Institute, Rutgers  
University  
190 Freelinghuysen Road, Piscataway, NJ 08854, USA  
Tel: 732 445 3801  
Fax: 732 445 5735  
Email: bharti@waksman.rutgers.edu  
Seq primer: T7  
Class: BAC ends  
High quality sequence start: 24.  
Location/Qualifiers  
1. .1025  
/organism="Zea mays subsp. mays"  
/mol\_type="genomic DNA"  
/cultivar="B73"  
/sub\_species="mays"  
/db\_xref="taxon:4578"  
/clone="ZMMBHC0120G04"  
/lab\_host="E. coli DH10B"  
/clone\_lib="ZMMBHC (EcoRI)"  
/note="Vector: pTARBAC2.1; Site\_1: EcoRI; Site\_2: EcoRI"

FEATURES  
source  
1. .1025

ORIGIN

Query Match	17.0%;	Score 899.6;	DB 29;	Length 1025;
Best Local Similarity	98.2%;	Pred. No. 1.2e-208;		
Matches	931;	Conservative 0;	Mismatches 14;	Indels 3; Gaps 2;
QY	2701	GCTGCTAGACGTAATCATGTCATACACTGTTTCTCTGTGTGAATTTGTTATTCGGCTCACCA	2760	
Db	78	GCAAGCTTGGCGTAATCATGTCATACACTGTTTCTCTGTGTGAATTTGTTATTCGGCTCACCA	137	
QY	2761	ATTCCACACAACATACGAGCGGAAGCATAAAGTGTAAAGCCTTGGGCTGCTTAATGAGTG	2820	
Db	138	ATTCCACACAACATACGAGCGGAAGCATAAAGTGTAAAGCCTTGGGCTGCTTAATGAGTG	197	
QY	2821	AGCTAACTCAATTAATTGGTTTGGCTCTCACTGCCCGCTTTCCAGTTCGGAAACCTGTCTG	2880	
Db	198	AGCTAACTCAATTAATTGGTTTGGCTCTCACTGCCCGCTTTCCAGTTCGGAAACCTGTCTG	257	
QY	2881	TGCCAGCTGCATTAATCAATCGGCCAACGGCGGGAGAGCGGTTTGCCTATTTGGCGC	2940	
Db	258	TGCCAGCTGCATTAATCAATCGGCCAACGGCGGGAGAGCGGTTTGCCTATTTGGCGC	317	
QY	2941	TCCTTCGGCTTCCTCGCTCACTGACTCGCTCGCTCGCTTCGGCTGCGCGCAGCGGTA	3000	
Db	318	TCCTTCGGCTTCCTCGCTCACTGACTCGCTCGCTCGCTTCGGCTGCGCGCAGCGGTA	377	
QY	3001	TCAGCTCAC--TCAAAGCGGTAATACGGTTATCCACAGATCAGGGATTAACCCAGAAA	3059	
Db	378	TCAGCTCACTTTATAGCGGTAATACGGTTATCCACAGATCAGGGGATTAACCCAGAAA	437	
QY	3060	GAACATGTGAGCAAAAGGCCAGCAAAAGGCCAGGAACCGTAAAGAACGCCGTTGCTGGC	3119	
Db	438	GAACATGTGAGCAAAAGGCCAGCAAAAGGCCAGGAACCGTAAAGAACGCCGTTGCTGGC	497	
QY	3120	GTTTTTCATFAGGTCGCGCCCTGACGAGCATCAAAAATCGACGCTCAAAGTCAGAG	3179	
Db	498	GTTTTTCATFAGGTCGCGCCCTGACGAGCATCAAAAATCGACGCTCAAAGTCAGAG	557	
QY	3180	GTGGCGAAACCCACAGGACTATAAGATACAGCGGTTTCCCGCTGGAAGCTCCCTCGT	3239	
Db	558	GTGGCGAAACCCACAGGACTATAAGATACAGCGGTTTCCCGCTGGAAGCTCCCTCGT	617	
QY	3240	GCCTCTCTCTGTTCCGACCCCTGCGGTTACCGGATACCTGTCCGCGCTTCTCCCTTCGGG	3299	
Db	618	GCCTCTCTCTGTTCCGACCCCTGCGGTTACCGGATACCTGTCCGCGCTTCTCCCTTCGGG	677	
QY	3300	AAGCGTGGCGTTTCTCATAGCTCAGCTGTAGGTATCTCAGTTCGGTGTAGTGTCTTCG	3359	
Db	678	AAGCGTGGCGTTTCTCATAGCTCAGCTGTAGGTATCTCAGTTCGGTGTAGTGTCTTCG	737	
QY	3360	CTCCAAAGCTGGGCTGTGTGCAGAAACCCCGGTTACGCCGACCGCTGCGCGCTTATCCGG	3419	
Db	738	CTCCAAAGCTGGGCTGTGTGCAGAAACCCCGGTTACGCCGACCGCTGCGCGCTTATCCGG	797	
QY	3420	TAACTATCGTCTTGTAGTCCAAACCGGTAAAGACACGACTTATCGCCACTGGCAGACCCAC	3479	
Db	798	TAACTATCGTCTTGTAGTCCAAACCGGTAAAGACACGACTTATCGCCACTGGCAGACCCAC	857	
QY	3480	TGTTAACAGATTTAGCAGAGCGAGGTATGTAGCGGTGCTACAGAGTTCTTGAAGTGGTG	3539	
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QY	3540	GCTTAACACTCGGCTACACTAGAGAACAGTAATTTGGTATCTCGCTCTCTCTGAAGCCAGT	3599	
Db	918	GCCTAACTACGGCTACACTAGAGAACAGTAATTTGGTATCTCGCTCTCTCTGAAGCCAGT	977	
QY	3600	TACCTTCGG--AAAAAGAGTTGTAGTCTTGTATCCGGCAAAACAAACC	3645	
Db	978	TACCTTCGGAAAGAGTTGGGAAGCTTGTATCCGGCAAAACAAACC	1025	

RESULT 10  
CG392995  
LOCUS

DEFINITION	ZMMBB00004E12f ZMMBBc (EcoRI) Zea mays subsp. may's genomic clone
ACCESSION	ZMMBB00004E12 5', genomic survey sequence.
VERSION	CG392995
KEYWORDS	CG392995.1 GI:34336220
SOURCE	GSS.
ORGANISM	Zea mays subsp. mays (maize)
REFERENCE	Zea mays subsp. mays Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea. 1 (bases 1 to 996)
AUTHORS	Bharti,A.K., Young,S., Kavchok,S., Keizer,G., Bronzino,A.C., Rouard,X., Fuku,G., Yu,Y., Wang,R. and Messing,J. Sequencing of the maize genome at PGIR (2003b) Unpublished (2003) Contact: Bharti.A.K. Dr.Joachim Messing's lab
TITLE	The Plant Genome Initiative at Rutgers, Waksman Institute, Rutgers
JOURNAL	University
COMMENT	190 Frelinghuysen Road, Piscataway, NJ 08854, USA Tel: 732 445 3801 Fax: 732 445 5735 Email: bharti@waksman.rutgers.edu Seq primer: T7 Class: BAC ends High quality sequence start: 11. Location/Qualifiers 1..996 /organism="Zea mays subsp. mays" /mol_type="genomic DNA" /cultivar="B73" /sub_species="mays" /db_xref="taxon:4578" /clone="ZMMBB00004E12" /lab_host="E. coli DH10B" /clone_lib="ZMMBBc (EcoRI)" /note="vector: pTARBAC2.1; Site 1: EcoRI; Site 2: EcoRT"
FEATURES	source

ORIGIN	/note="vector: pTBAC2.1; Site_1: EcoRI; Site_2: EcoRI"									
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Best Local Similarity	98.7%;	Pred.	No. 1.9e-208;							
Matches	906;	Conservative	0;	Mismatches	12;	Indels	0;	Gaps	0;	
QY	2701	GC	TG	CT	CA	G	CT	CA	G	CT
DB	79	G	C	A	A	G	T	G	T	T
QY	2761	A	T	T	C	C	A	T	T	T
DB	139	A	T	T	C	C	A	T	T	T
QY	2821	A	G	T	T	G	G	T	T	T
DB	199	A	G	T	T	G	G	T	T	T
QY	2881	T	G	C	A	G	T	T	T	T
DB	259	T	G	C	A	G	T	T	T	T
QY	2941	T	C	T	T	C	G	T	T	T
DB	319	T	C	T	T	C	G	T	T	T
QY	3001	T	C	A	G	T	T	T	T	T
DB	379	T	C	A	G	T	T	T	T	T
QY	3061	A	A	C	A	T	G	A	A	A
DB	439	A	A	C	A	T	G	A	A	A
QY	3121	T	T	T	T	T	T	T	T	T

CG392995  
LOCUS  
CG392995  
996 bp  
DNA  
linear  
GSS 22-SEP-2003

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 3181 TGCGGAAACCCGACAGGACTATAAGATACAGGCGTTTCCCTCGGAAAGCTCCCTCGTG 3240  
 559 TGCGGAAACCCGACAGGACTATAAGATACAGGCGTTTCCCTCGGAAAGCTCCCTCGTG 618  
 3241 CGCTCTCTGTTCCGACCTCGGCTTACGGATACCTGTCGCGCTTCTCCCTCGGGA 3300  
 619 CGCTCTCTGTTCCGACCTCGGCTTACGGATACCTGTCGCGCTTCTCCCTCGGGA 678  
 3301 AGCGTCGCGCTTCTCATAGCTCACGCTGTAGTATCTCAGTTCGGTGTAGTTCGCTCGC 3360  
 679 AGCGTCGCGCTTCTCATAGCTCACGCTGTAGTATCTCAGTTCGGTGTAGTTCGCTCGC 738  
 3361 TCCAACTGCGGTGTGTGACGAAACCCCGGTTTACGCGGACCGCTTCGCGCTTATCCGGT 3420  
 739 TCCAACTGCGGTGTGTGACGAAACCCCGGTTTACGCGGACCGCTTCGCGCTTATCCGGT 798  
 3421 AACTATCGTCTGAGTCCAAACCGGTAAGACAGCACTTATCGCACTGGCAGCAGCACT 3480  
 799 AACTATCGTCTGAGTCCAAACCGGTAAGACAGCACTTATCGCACTGGCAGCAGCACT 858  
 3481 GGTAAACAGATTACGAGGAGGATGTAGGCGGTGTACAGAGTCTTTGAAGTGTGG 3540  
 859 GGTAAACAGATTACGAGGAGGATGTAGGCGGTGTACAGAGTCTTTGAAGTGTGG 918  
 3541 CCTAATACCGGTACACTAGAAAGACAGTATTTGGTATCTGCGCTCTGTGAAGCCAGTT 3600  
 919 CCTAATACCGGTACACTAGAAAGACAGTATTTGGTATCTGCGCTCTGTGAAGCCAGTT 978  
 3601 ACCTTCGGAAGAAAGAGTT 3618  
 979 TACCTCGGAAAGAGGT 996

RESULT 11  
 CK291799/c  
 LOCUS  
 DEFINITION  
 EST754513 Nicotiana benthamiana mixed tissue cDNA library,  
 normalized, full-length Nicotiana benthamiana cDNA clone NBMC477 5',  
 end, mRNA sequence.  
 CK291799  
 CK291799.1 GI:39872608  
 EST.  
 KEYWORDS  
 SOURCE  
 ORGANISM  
 Nicotiana benthamiana  
 Nicotiana benthamiana  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
 asterids; lamids; Solanales; Solanaceae; Nicotiana.  
 1 (bases 1 to 933)  
 Buell,C.R., Hart,A., Zismann,V., Karamycheva,S.A., Day,B.,  
 Staskiewicz,B., Jin,H. and Baker,B.  
 Generation of EST sequences from Nicotiana benthamiana  
 Unpublished (2003)  
 Other ESTs: EST754514  
 Contact: Robin Buell  
 The Institute for Genomic Research  
 9712 Medical Center Dr, Rockville, MD 20850, USA  
 Email: potato-array@tigr.org  
 Clones can be requested from TIGR via potato@tigr.org  
 Seq primer: ATT TAG GTG ACA CTA TAG.  
 Location/Qualifiers  
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 /note="vector: pCMVSPORT6.1; Site\_1: EcoRI; Site\_2: NotI;

supplier: RNA was isolated from Nicotiana benthamiana  
 tissues that include callus, roots from liquid culture  
 grown plants, heat-stressed leaves (38 C, 3 hr and 6 hr),  
 cold-stressed leaves (5 C 3 hr, 6hr), and pathogen  
 challenged leaves (Pseudomonas syringae pv tomat 12 hr;  
 Xanthomonas campestris pv campestris 12 hr, 18hr;  
 Pseudomonas syringae pv phaseolicola 18hr, and Xanthomonas  
 campestris pv vesicatoria 18hr). RNA was isolated from  
 these tissues and pooled in approximately equal molar  
 amounts."

Query Match 16.8%; Score 886.4; DB 14; Length 933;  
 Best Local Similarity 99.9%; Pred. No. 2e-205;  
 Matches 887; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4044 GCCCAACCTTTCATAGAGCGCGGTGGAATTCGAAATCTCGTATGCGCAGGTGGCGGT 4103  
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 QY 4104 CGCTTGGTCCGTCATTTTCGAACCCCGAGTCCCGCTCAGAAGAACTCGTCAAGAAGCGGA 4163  
 DB 873 CGCTTGGTCCGTCATTTTCGAACCCCGAGTCCCGCTCAGAAGAACTCGTCAAGAAGCGGA 814  
 QY 4164 TAGAAGCGGATGCGCTGCGAATCGGAGCGCGGATACCGTAAAGACAGAGAGCGGTCA 4223  
 DB 813 TAGAAGCGGATGCGCTGCGAATCGGAGCGCGGATACCGTAAAGACAGAGAGCGGTCA 754  
 QY 4224 GCCCATTCGCGCAAGCTCTTCAGCAATATCAGGGTAGCCACCGTATGTCCTGATAG 4283  
 DB 753 GCCCATTCGCGCAAGCTCTTCAGCAATATCAGGGTAGCCACCGTATGTCCTGATAG 694  
 QY 4284 CGGTCCGCCACACCCAGCGGCCACAGTCCGATGAATCCAGAAAAGCGGCCATTTTCCACC 4343  
 DB 693 CGGTCCGCCACACCCAGCGGCCACAGTCCGATGAATCCAGAAAAGCGGCCATTTTCCACC 634  
 QY 4344 ATGATATTCGCGCAAGCGGATCGCCATGGGTTCACGACGAGATCTCTCGCGTCGGGATG 4403  
 DB 633 ATGATATTCGCGCAAGCGGATCGCCATGGGTTCACGACGAGATCTCTCGCGTCGGGATG 574  
 QY 4404 CGGCGCTTGAAGCTTGGCGAAACAGTTTGGCTGGGCGGAGCCCTGATGCTCTTCGTCGAGA 4463  
 DB 573 CGGCGCTTGAAGCTTGGCGAAACAGTTTGGCTGGGCGGAGCCCTGATGCTCTTCGTCGAGA 514  
 QY 4464 TCATCTGTATCGCAAGACCGGCTTCCATCCGAGTACGTCTCGCTCGATGCGATGTTTC 4523  
 DB 513 TCATCTGTATCGCAAGACCGGCTTCCATCCGAGTACGTCTCGCTCGATGCGATGTTTC 454  
 QY 4524 GCTTGGTGTGCAATGGGCGAGTAGCCGATCAAGCGTATGACGCCCGCGCATTTGCATCA 4583  
 DB 453 GCTTGGTGTGCAATGGGCGAGTAGCCGATCAAGCGTATGACGCCCGCGCATTTGCATCA 394  
 QY 4584 GCCATGATGATATCTTCTCGGAGGACGAGGTGAGATGACAGAGATCTCTGCCCCCGGC 4643  
 DB 393 GCCATGATGATATCTTCTCGGAGGACGAGGTGAGATGACAGAGATCTCTGCCCCCGGC 334  
 QY 4644 ACTTCGCCCAATAGCAGCCAGTCCCTTCCCGCTTCAGTGACAAAGCTCGAGCAGAGTCCG 4703  
 DB 333 ACTTCGCCCAATAGCAGCCAGTCCCTTCCCGCTTCAGTGACAAAGCTCGAGCAGAGTCCG 274  
 QY 4704 CAAGAAACGCCCGCTGTCGGCGAGCCAGATAGCCGCGTGCCTGCTCTGAGTTCATTC 4763  
 DB 273 CAAGAAACGCCCGCTGTCGGCGAGCCAGATAGCCGCGTGCCTGCTCTGAGTTCATTC 214  
 QY 4764 AGGCGACCGGACAGTCCGCTTCACAAAAGAACCGGGCGCCCTCGCTGACAGCCGG 4823  
 DB 213 AGGCGACCGGACAGTCCGCTTCACAAAAGAACCGGGCGCCCTCGCTGACAGCCGG 154  
 QY 4824 AACACGGCGGATCAGAGCAGCCGATTTGTGTGTGCCAGTATAGCCGAAATAGCCTC 4883  
 DB 153 AACACGGCGGATCAGAGCAGCCGATTTGTGTGTGCCAGTATAGCCGAAATAGCCTC 94  
 QY 4884 TCCACCCCAAGCGCGGAGAACCTCGGTGCAATCCATCTTTGTCATC 4931

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Db      93  TCACCCAGCGCGGAGACCTGGTGCATTCATCTTGTTCAATC 46
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ZMMBBc0004E11 5', genomic survey sequence.
CG392916
CG392916.1 GI:343336141
GSS.
Zea mays subsp. mays (maize)
Zea mays subsp. mays
Zea mays subsp. mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.
REFERENCE 1 (bases 1 to 1021)
AUTHORS Bharti.A.K., Young,S., Kavchok,S., Keizer,G., Bronzino,A.C.,
Rouzaud,K., Fuks,G., Yu,Y., Wing,R. and Messing,J.
TITLE Sequencing of the maize genome at PGIR (2003b)
JOURNAL Unpublished (2003)
COMMENT Contact: Bharti.A.K.
Dr.Joachim Messing's lab
The Plant Genome Initiative at Rutgers, Waksman Institute, Rutgers
University
190 Frelinghuysen Road, Piscataway, NJ 08854, USA
Tel: 732 445 3801
Fax: 732 445 5735
Email: bharti@waksman.rutgers.edu
Seq primer: T7
Class: BAC ends.
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Query Match      16.7%; Score 883.6; DB 29; Length 1021;
Best Local Similarity 96.1%; Pred. No. 1e-204;
Matches 917; Conservative 0; Mismatches 34; Indels 3; Gaps 1;
QY      2701  GCTGCTAGACGTAATCATGTCATAGCTGTTTCTGCTGTGAATTTGTTATCCGCTCACA 2760
Db      67  GCAGCTTGGCGTAATCATGTCCTAGCTGTTTCTGCTGTGAATTTGTTATCCGCTCACA 126
QY      2761  ATTCACACACATACGAGCGGAGCATAAAGTAAAGCTGGGCTGCTATGAGTG 2820
Db      127  ATTCACACACATACGAGCGGAGCATAAAGTAAAGCTGGGCTGCTATGAGTG 186
QY      2821  AGCTACTCATTAATTTGCGTTTTCGCTCACTGCGCGCTTTCCAGTCCGGAAACCTCTCG 2880
Db      187  AGCTACTCATTAATTTGCGTTTTCGCTCACTGCGCGCTTTCCAGTCCGGAAACCTCTCG 246
QY      2881  TGCAGCTGATTAATGAATCGGCCAACGCGCGGGAGAGCGGTTTGCCTATTGGGCGC 2940
Db      247  TGCAGCTGATTAATGAATCGGCCAACGCGCGGGAGAGCGGTTTGCCTATTGGGCGC 306
QY      2941  TCTTCCGCTTCTCGCTCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 3000
Db      307  TCTTCCGCTTCTCGCTCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 366
QY      3001  TCAGCTCACTCAAGAGCGGTAATACGGTTATCCACAGAAATCAGGGGATACGCGAGAAAG 3060
Db      367  TCAGCTCACTCAAGAGCGGTAATATTGTTATCCACAGAAATCAGGGGATACGCGAGAAAG 426
QY      3061  AACATGTGAGCAAAAGGCCAGCAAAAGGCCAGCAAAAGGCCAGCAAAAGGCCAGCAAAAGGCC 3120
Db      427  AACATGTGAGCAAAAGGCCAGCAAAAGGCCAGCAAAAGGCCAGCAAAAGGCCAGCAAAAGGCC 486
QY      3121  TTTTTCATAGCTCGCCCGCTTACCGGATACCTGTCCGCTTCTCTCTCTCTCTCTCTCTCTCT 3180
Db      487  TTTTTCATAGCTCGCCCGCTTACCGGATACCTGTCCGCTTCTCTCTCTCTCTCTCTCTCTCT 546
QY      3181  TGGCGAAACCCGACAGGACTATAAAGATACACAGGCGTTTCCCGCTGGAAGCTCCCTCGTG 3240
Db      547  TGGCGAAACCTCGACAGGACTATAAAGATACACAGGCGTTTCTCTCTGGAAGCTCTCTCGTG 606
QY      3241  CGCTCTCTCTTCCGACCTTACCGGATACCTGTCCGCTTCTCTCTCTCTCTCTCTCTCTCTCT 3300
Db      607  CGCTCTCTCTTCCGACCTTACCGGATACCTGTCCGCTTCTCTCTCTCTCTCTCTCTCTCTCT 666
QY      3301  AGCGTGGCGCTTCTCATAGCTACGCTGTAGTATCTCAGTTCGCTGTAGTTCGCTTCGC 3360
Db      667  AGCGTGGCGCTTCTCATAGCTACGCTGTAGTATCTCAGTTCGCTGTAGTTCGCTTCGC 726
QY      3361  TCCAGCTGGGCTGTGTCAGCAAGACCCCGCTTACGCGCGGCTGCGCTTATCCGCT 3420
Db      727  TTCAGCTGGGCTGTGTCAGCAAGACCCCGCTTCTCTGTTCAGCTCGACTGCTGCGCTTATCCG 786
QY      3421  AACTATCGTCTTGTAGTCCAAACCCGCTTAAGACACAGCACTTATCGCCACTGCGAGCCACT 3480
Db      787  AACTATCGTCTTGTAGTCCAACTCGTAAACACAGCACTTATCGTACTGCGAGCACTACT 846
QY      3481  GGTAAACAGGATTAGCAGAGCGAGGTATGTAGCGGCTGTACAGAGTCTTCTGAAGTGGTG 3540
Db      847  GGTAAACAGGATTAGCAGAGCGAGGTATGTAGCGGCTGTACAGAGTCTTCTGAAGTGGTG 906
QY      3541  CCTAAGTACGGCTACACTAGAGAACAGTATTTGGTATCTCGCTCTCTCTCTCTCTCTCTCT 3600
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QY      3601  ACCTTCGGAAAAAGAGTTGGTA---GCTCTTGTATCCGGCAAAACAAACCAACCGCT 3651
Db      967  ACCTTCGGAAAAAGAGTTGGTAAGCTTCTTGAATTCGGGCAAAACAAACCAACCGCT 1020
RESULT 13
CB686151/c
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DEFINITION Bn01b_AAPC_ECORC_transgenic_Brassica_napus overexpressing BNCBF17_c
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            mRNA sequence.
ACCESSION  CB686151
VERSION    CB686151.1 GI:29689876
KEYWORDS   EST.
SOURCE     Brassica napus (rape)
ORGANISM  Brassica napus
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            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            rosids; eurosids II; Brassicales; Brassicaceae; Brassica.
REFERENCE  1 (bases 1 to 925)
AUTHORS   Singh,J., Allard,G., Tinker,N., Robert,L., Lacroix,C., De Moors,A.,
            Chagnon,J., Farah,S., Couroux,P. and Hattori,J.
TITLE     Expressed Sequence Tags from constitutively frost tolerant
            transgenic Brassica napus overexpressing BNCBF17
JOURNAL   Unpublished (2002)
COMMENT   Contact: Singh,J.A.
            Eastern Cereal and Oilseed Research Centre
            Agriculture and Agri-food Canada
            KW Neatby Bldg., Central Experimental Farm, Ottawa, Ontario, K1A
            0C6, Canada
            Tel: (613) 759-1662
            Fax: (613) 759-1701
            Email: singhja@agr.ca.
            Location/Qualifiers
            1..925
            /organism="Brassica napus"
FEATURES             source

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/mol_type="mRNA"
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/dev_stage="3 weeks seedling grown at room temperature"
/clone_lib="Bn01b AAFRC R00RC transgenic Brassica napus_ove
repressing BNCBF17 constitutively frost tolerant"
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collected at 9 am and immediately frozen."

```

## ORIGIN

	Query Match	16.6%;	Score 875;	DB 14;	Length 925;
	Best Local Similarity	98.6%;	Pred. No. 1.2e-202;		
	Matches 886;	Conservative	6;	Mismatches	1; Gaps 1;
Qy	2701	GCCTGCTAGACGTAATCATAGCTCATAGCTGTTTCCCTGTGTGAAATTTGTTATCCGCTCACA	2760		
Db	898	GCGGCTTGCGGTAAATCATAGCTCATAGCTGTTTCTGTGTGAAATTTGTTATCCGCTCACA	840		
Qy	2761	ATTCCACACAACATACGAGCGGAAGCATAAAGTGTAAAGCCTGGGGTGCCTAATACAGTG	2820		
Db	839	ATTCCACACAACATACGAGCGGAAGCATAAAGTGTAAAGCCTGGGGTGCCTAATACAGTG	780		
Qy	2821	AGCTAACTCACATTAATTTGGTTTGGCTCACTGCCCGCTTTCAGTCGGGAAACCTGTG	2880		
Db	779	AGCTAACTCACATTAATTTGGTTTGGCTCACTGCCCGCTTTCAGTCGGGAAACCTGTG	720		
Qy	2881	TGCCAGCTGCATTAATGAATTCGCGCAACGCGCGGGAGAGCGGTTTGGTATTGGCGC	2940		
Db	719	TGCCAGCTGCATTAATGAATTCGCGCAACGCGCGGGAGAGCGGTTTGGTATTGGCGC	660		
Qy	2941	TCCTTCGCTTCTCGCTCACTGACTCGCTCGCTCGCTCGCTCGCTCGCTCGCTCGCTCGCT	3000		
Db	659	TCCTTCGCTTCTCGCTCACTGACTCGCTCGCTCGCTCGCTCGCTCGCTCGCTCGCTCGCT	600		
Qy	3001	TCAGCTCACTCAAAGCGGTAAATACGGTTATCCACAGAAATCAGGGGATACGCAGGAAG	3060		
Db	599	TCAGCTCACTCAAAGCGGTAAATACGGTTATCCACAGAAATCAGGGGATACGCAGGAAG	540		
Qy	3061	AACATGTGACGAAAGCGCAGCAAAAGCGCAGGAACCGTAAAGGCGCGGTTGCTGGCG	3120		
Db	539	AACATGTGACGAAAGCGCAGCAAAAGCGCAGGAACCGTAAAGGCGCGGTTGCTGGCG	480		
Qy	3121	TTTTTCCATAGGCTCCGCCCCCTTGACGAGCATCACAAAATCGACGCTCAAGTCAGAGG	3180		
Db	479	TTTTTCCATAGGCTCCGCCCCCTTGACGAGCATCACAAAATCGACGCTCAAGTCAGAGG	420		
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Db	419	TGGCGAAACCGCAGCAGCACTATAAGATACGAGCGTTTCCCTCTGAAAGCTCCCTCGTG	360		
Qy	3241	CGCTCTCTGTTCCGACCGCTGCGCGCTTACCGGATACCTGTCCGCGCTTCTCCCTTCGGGA	3300		
Db	359	CGCTCTCTGTTCCGACCGCTGCGCGCTTACCGGATACCTGTCCGCGCTTCTCCCTTCGGGA	300		
Qy	3301	AGCGTGGCGCTTCTCATAGCTCAGCTGTAGGTATCTCAGTTCGGTGTAGGTGCTGTCG	3360		
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Qy	3361	TCCAAGCTGGGCTGTGTGTCAGCAAGAACCCCGCTTTCAGCCCGACCGCTGCGCTTATCCGGT	3420		
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Db 119 GGTAAACAGATTATCAGACGCGTATGTAGGCGGTCTACAGAGTTCTTSAAGTGCTGG 60

QY 3541 CCTAAGTCACGGCTACTACTAGAAGAACAGTATTTGGTATCTGCCTCTGCCTGAAGCCAGT 3599  
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | : | | | | | : | | | | | : | | | | | : | | | | | :  
Db 59 CTTTAACCTACGGSTACACTAGAGAAACAGTATTTGGTATCTGCCTCTGCCTGAAGCCAGT 1

RESULT 14  
CF269652 1073 bp mRNA linear EST 13-AUG-2003  
LOCUS Fcylcold844 Fragilariopsis cylindrus SMART cDNA library (Clontech)  
DEFINITION Fragilariopsis cylindrus cDNA clone Antarctic 5', mRNA sequence.  
ACCESSION CF269652  
VERSION CF269652.1 GI:33631539  
KEYWORDS EST.  
SOURCE Fragilariopsis cylindrus  
ORGANISM Fragilariopsis cylindrus  
Eukaryota; stramenopiles; Bacillariophyta; Bacillariophyceae;  
Bacillariophycidae; Bacillariales; Bacillariaceae; Fragilariopsis  
1 (bases 1 to 1073)  
Mock.T. and Valentin.K.  
EST analysis of freezing tolerance in the Antarctic diatom  
Fragilariopsis cylindrus: Detection of numerous cold adaptation  
related genes and gene transfer events  
Unpublished (2003)  
JOURNAL Contact: Mock T  
COMMENT Biological Oceanography  
Alfred-Wegener-Institute for Polar and Marine Research  
Am Handelshafen 12, D-27570 Bremerhaven, Germany  
Tel.: +49 471 4831 1893  
Fax: +49 471 4831 1425  
Email: tmoekawi-bremerhaven.de  
sequence with unknown function  
PCR Primers  
FORWARD: 5'lambdaTriplex2  
BACKWARD: 3'lambdaTriplex2  
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denaturation and subsequent 20 cycles at 95oC (2min) and  
68oC (6min). After SfiI digestion the cDNA was  
fractionated with CHROMA Spin-400 columns. These cDNAs  
were ligated overnight into pTriplex2 vectors."

ORIGIN  
Query Match 16.4%; Score 866.2; DB 14; Length 1073;  
Best Local Similarity 96.4%; Pred. No. 1.9e-200;  
Matches 927; Conservative 0; Mismatches 28; Indels 7; Gaps 4

QY 2839 GGTTTCGCTCACTGCCGCTTTCCAGTCGGAAACCTGTCTGTGCAGTCGATTAAATGA 2899  
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Db 2899 ATCGGCCAACGGCGGGGAGAGCGGTTTGGCTATTGGCGCTCTTCGCTTCCCTCGCTC 295  
61 ATCGGCCAACGGCGGGGAGAGCGGTTTGGCTATTGGCGCTCTTCGCTTCCCTCGCTC 120

QY 2959 ACTGACTCGCTCGCTCGCTCGCTTTCGGCTTCGGCTCGCGCGAGCGGTATCATGTCAC 301  
Db 121 ACTGACTCGCTCGCTCGCTCTTTTCGGCTTCGGCTCGCGCGAGCGGTATCATGTCAC 180

QY 3019 GTAATA CGGTTATTCACA GAATCAGGGGATTAACGAGGAAGNACATGTGAGCAAAGGC 307

OPTICN

Query Match 16.4%; Score 866.2; DB 14; Length 1073;  
Best Local Similarity 96.4%; Pred. No. 1.9e-200;  
Matches 927; Conservative 0; Mismatches 28; Indels 7; Gaps 4

	Qy	2839	GCGTTGGCTCACTGCCGCTTCCAGTCGGAAACCTGTGTCGCAGCTGCATTAAATGA	2887
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	Qy	2899	ATCGGCCAACGCGGGGAGAGCGGTTTGGGTATTGGCGCTCTTTCGGCTCCTCGCTC	295
	Db	61	ATCGGCCAACGCGGGGAGAGCGGTTTGGGTATTGGCGCTCTTTCGGCTCCTCGCTC	120
	Qy	2959	ACTGACTCGCTCGCTCGGTCGGTTCGGTCGGCGAGCGGTATCAGTCACTCAAAGGCG	301
	Db	121	ACTGACTCGCTCGCTCGGTCCTTCGGCTCGCGGAGCGGTATCAGCTCACTCAAAGGCG	180
	Ov	3019	GTAATA CGGTTTATCCACA GATCAGGGGATACG CAGGAAGA A CATGTG CAGGAAGGC	307

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Db 181 GTAAACGCTTATCACAGAAATCAGGGGATACGAGGAAAGAAATGTGACAAAAGGC 240
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Db 361 CTATAAGATACCGAGCGTTTCCCGCTGGAAGCTCCCTGCGGTCTCTCTTCCGACC 420
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Db 421 CTGCGGCTTACCGGATACCTGTCGCCCTTTCCTCCCTCGGGAAGCGTGGCGTTTCTCAT 480
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Db 481 AGCTCACGCTGATGATCTCAGTTTCGGTGTAGTTCGTTCCGCTCAAGCTGGGCTGTGTG 540
QY 3379 CACGAACCCCGCTTCAGCCGACCGCTGCGCTTATCCGGTAACTATCGTCTTGAGTCC 3438
Db 541 CACGAACCCCGCTTCAGCCGACCGCTGCGCTTATCCGGTAACTATCGTCTTGAGTCC 600
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QY 3672 TTGAAGCAGAGATTAACGCGAGAAAGGATCTCAAGAGATCTTTGATCTTTTC 3731
Db 841 TTGAAGCAGAGATTAACGCGAGAAAGGATCTCAAGAGATCTTTGATCTTTTC 900
QY 3732 TACGGGCTTGACGCTCAGTGGAGCAAACTCAGTTAAGGATTTGGTCAAGATT 3791
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RESULT 15
CG835880 1056 bp DNA linear GSS 12-NOV-2003
LOCUS ZMMBbc0212F14f ZMMBbc (EcoRI) Zea mays subsp. mays genomic clone
DEFINITION ZMMBbc0212F14 5', genomic survey sequence.
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ACCESSION CG835880
VERSION CG835880.1 GI:38300279
KEYWORDS GSS.
SOURCE Zea mays subsp. mays (maize)
ORGANISM Zea mays subsp. mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.
1 (bases 1 to 1056)
Bharti,A.K., Young,S., Kavchok,S., Keizer,G., Bronzino,A.C.,
Zohovetz,V., Fuks,G., Yu,Y., Wing,R. and Messing,J.
Sequencing of the maize genome at pGIR (2003c)
```

JOURNAL  
COMMENT

Unpublished (2003)  
Contact: Bharti, A. K.  
Dr. Joachim Messing's lab  
The Plant Genome Initiative at Rutgers, Waksman Institute, Rutgers  
University  
190 Frelinghuysen Road, Piscataway, NJ 08854, USA  
Tel: 732 445 3801  
Fax: 732 445 5735  
Email: bharti@waksman.rutgers.edu  
Seq primer: 17

Class: BAC ends

High quality sequence start: 74.

FEATURES  
source

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## ORIGIN

Query Match 16.1%; Score 849; DB 29; Length 1056;  
Best Local Similarity 95.8%; Pred. No. 3.1e-196;  
Matches 936; Conservative 0; Mismatches 35; Indels 6; Gaps 6;  
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QY 3300 AAGGTGGCGCTTCTCATAGCTACGCTGATGATCTCAGTTTCGGTGTAGTGTCTG 3359  
Db 680 AAGGTGGCGCTTCTCATAGCTCAGCTGTAGTATCTCAGTTTCGGTGTAGTGTCTG 739



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